

GenCore version 5.1.7
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M protein - protein search, using sw mode!
run on: March 10, 2006, 19:52:00 / Search time 106.537 Seconds
(without alignments)
1187.771 Million cell updates/sec
title: US-10-781-181-3
perfect score: 1540
sequence: 1 MSCLMVERCGELIFENPDQN GTWDFDFIIFFDRLTNGNSLV 288
scoring table: BLOSUM62;
GapOp 10.0 , Gapext 0.5
searched: 2443163 seqs, 439378781 residues
total number of hits matching chosen parameters: 2443163

ATTACHMENTS

RESULT 1
 AAY93568
 ID AAY93568 standard; protein; 288 AA.
 XX
 AAY93568;
 AC
 XX
 DDT 25-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of a human phosphodiesterase enzyme.
 XX
 KW Phosphodiesterase; PDE-XIV; human; enzyme.
 KW
 OS Homo sapiens.

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Query		Length	DB	ID	Description	
		Score	Match					
1	1540	100.0	288	3	AAY93568	Amino aci	Aay93568 Amino aci	
	2	1430	92.9	268	3	AAV93593	Amino aci	Aay93593 Amino aci
	3	1430	92.9	450	3	AAV93569	Amino aci	Aay93569 Amino aci
	4	1430	92.9	450	4	AAU08675	Human pho	Aau08675 Human pho
	5	1430	92.9	450	4	AAGT9815	Human typ	Aag78915 Human typ
	6	1430	92.9	450	8	ADP79549	Human pho	Adp79549 Human pho
	7	1376	89.4	446	3	AAY93567	Amino aci	Aay93567 Amino aci
	8	1356	88.1	445	3	AAV93573	Amino aci	Aay93573 Amino aci
	9	1356	88.1	446	3	AAV93574	Amino aci	Aay93574 Amino aci
	10	1356	88.1	451	3	AAV93575	Amino aci	Aay93575 Amino aci
	11	1337	86.8	437	3	AAV93572	Amino aci	Aay93572 Amino aci
	12	1280	83.1	320	4	AAB816504	Human sho	Aab816504 Human sho
	13	1280	83.1	320	8	ADJS8906	Human cyc	Adj8906 Human cyc
	14	1280	83.1	502	5	ABB09005	Human pho	Abb09005 Human pho
	15	1280	83.1	502	8	ADJ58904	Human cyc	Adj58904 Human cyc
	16	1262	81.9	502	4	AAB816503	Human lon	Aab816503 Human lon
	17	1259.5	81.8	413	3	AAV93571	Amino aci	Aay93571 Amino aci
	18	1145	74.4	391	4	AAU08676	Human pho	Aau08676 Human pho
	19	980	63.6	335	9	ADY50214	Human pde	Ady50214 Human pde
	20	980	63.6	335	9	ADZ66770	Human pde	Adz66770 Human pde
	21	913	59.3	456	5	AAB24530	Mouse pde	Aab24530 Mouse pde
	22	907	58.9	424	5	AAU97227	Human cyc	Aau97227 Human cyc
	23	907	58.9	432	4	AAU16967	Human nov	Aau16967 Human nov

XX XX 23-DEC-1998; 98GB-00028603.
XX PR PR 17-SEP-1999; 99GB-00022123.
XX PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX PI Fidock M;
XX DR WPI; 2000-433274/38.
XX DR N-PSDB; AAA46650.
XX PT
PT
PT
XX Disclosure; Page 42-44; 104pp; English.
XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens against PDE-XIV and in assays to
CC assess the presence of antibodies against PDE-XIV and/or PDE-XIV variants and
CC isomers. The polypeptides may be used in the production of
CC monoclonal antibodies against PDE-XIV and/or PDE-XIV variants and
CC isomers.

CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))

XX Sequence 288 AA;

Query Match 100.0%; Score 1540; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 9_1e-16;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSCLMVERGEILFENPDONAKCYCMLGIDRLRGQTGYAERGSGYPFDFLRINNITYS 60
Db 1 MSCLMVERGEILFENPDONAKCYCMLGIDRLRGQTGYAERGSGYPFDFLRINNITYS 60
Qy 61 GEIGTKKKYKRLLSFQRYPHASRLRLGIPOAPLHLDDEYLQGARHMLSKVGNMWDFF 120
Db 61 GEIGTKKKYKRLLSFQRYPHASRLRLGIPOAPLHLDDEYLQGARHMLSKVGNMWDFF 120
Qy 121 LFDRLTNGSLVTLLCHLFNTGHJHHFCLDMYTLHRFLVMQEDYHSQNPYNAHAD 180
Db 121 LFDRLTNGSLVTLLCHLFNTGHJHHFCLDMYTLHRFLVMQEDYHSQNPYNAHAD 180
Qy 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
Db 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
Qy 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288
Db 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288

RESULT 2
AAV93593

ID AAV93593 standard; protein; 268 AA.
AC AAV93593;
XX DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a human phosphodiesterase enzyme.
KW Phosphodiesterase; PDE-XIV; enzyme.
XX Homo sapiens.

PN EP1018559-A1.

XX DR 12-JUL-2000.
XX PD 09-NOV-1999; 99EP-000308902.

XX PR 23-DEC-1998; 98GB-00028603.
XX PR 17-SEP-1999; 99GB-00022123.

PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.

XX PI Fidock M;

XX XX WPT; 2000-433274/3-B.

XX PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.
PT Disclosure; Page 87-88; 104pp; English.
PS XX

CC The present sequence represents a phosphodiesterase (PDE) enzyme. The CC phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with CC inappropriate PDE-XIV expression. For example, the polynucleotide be CC administered to treat diseases by rectifying mutations or deletions in a CC patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and CC their role in metabolism. The PDE-XIV polypeptides may be used as CC antigens in the production of antibodies against PDE-XIV and in assays to CC identify modulators (agonists and antagonists) of PDE-XIV expression and CC activity. The anti-PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies CC may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
CC XX Sequence 268 AA;
CC Query Match 92.9%; Score 1430; DB 3; Length 268;
CC Best Local Similarity 100.0%; Pred. No. 1_3e-149;
CC Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC Oy 1 MSCLMVERGEILFENPDONAKCYCMLGIDRLRGQTGYAERGSGYPFDFLRINNITYS 60
CC Db 1 MSCLMVERGEILFENPDONAKCYCMLGIDRLRGQTGYAERGSGYPFDFLRINNITYS 60
CC Qy 61 GEIGTKKKYKRLLSFQRYPHASRLRLGIPOAPLHLDDEYLQGARHMLSKVGNMWDFF 120
CC Db 61 GEIGTKKKYKRLLSFQRYPHASRLRLGIPOAPLHLDDEYLQGARHMLSKVGNMWDFF 120
CC Qy 121 LFDRLTNGSLVTLLCHLFNTGHJHHFCLDMYTLHRFLVMQEDYHSQNPYNAHAD 180
CC Db 121 LFDRLTNGSLVTLLCHLFNTGHJHHFCLDMYTLHRFLVMQEDYHSQNPYNAHAD 180
CC Qy 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
CC Db 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
CC Qy 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288
CC Db 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288
CC Qy 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
CC Db 181 VTQAMHCYKEPKLASFLTPLDIMGLLAAAHDVDHPQVNQPLIKTNHLANLYQMS 240
CC Qy 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288
CC Db 241 VLENHHWRSTIGMRESRLLAHLPKEMTGTWDFDIFLFLRITNGNSLV 288
CC RESULT 3
AAV93569
ID AAV93569 standard; protein; 450 AA.
XX AC AAV93569;
XX DT 25-SEP-2000 (first entry)
XX DE Amino acid sequence of a human phosphodiesterase enzyme.
XX KW Phosphodiesterase; PDE-XIV; human; enzyme.
XX OS Homo sapiens.
XX PN EP1018559-A1.
XX PD 12-JUL-2000.
XX PR 09-NOV-1999; 99EP-000308902.
XX PR 23-DEC-1998; 98GB-00028603.
XX PR 17-SEP-1999; 99GB-00022123.
XX PA (PFIZ) PFIZER LTD.
XX PA (PFIZ) PFIZER INC.
XX PN EP1018559-A1.
XX PD 12-JUL-2000.
XX PR 09-NOV-1999; 99EP-000308902.
XX PR 23-DEC-1998; 98GB-00028603.
XX PR 17-SEP-1999; 99GB-00022123.
XX PA (PFIZ) PFIZER LTD.
XX PA (PFIZ) PFIZER INC.

AAG78915 standard; protein; 450 AA.
 XX ID AAG78915 ;
 AC AAG78915 ;
 XX DT 19-DEC-2001 (first entry)
 XX DB Human type 7B phosphodiesterase, PDE7B; enzyme .
 XX OS Homo sapiens .
 XX PN JP2001238680-A.
 XX PD 04-SEP-2001 .
 XX PF 03-MAR-2000; 2000JP-00058159 .
 XX PR 03-MAR-2000; 2000JP-00058159 .
 XX PA (TANA) TANABE SEIYAKU CO.
 DR WPI: 2001-610057/70 .
 DR N-PSDB; AAI70009 .
 PT New phosphodiesterase for use in the development of inhibitors of high selectivity and drugs of low side effect .
 PS Claim 2; Page 12-14; 18pp; Japanese .
 CC The present sequence is the protein sequence for human type 7B phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the development of inhibitors of high selectivity and drugs of low side effects .
 CC Sequence 450 AA;
 SQ Best Local Similarity 100.0%; Score 1430; DB 4; Length 450;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Sequence 450 AA;

KW Human; phosphodiesterase 7B; PDE7B; cardiovascular-gen.; CNS-Gen.;
 KW gynaecological; haemostatic; respiratory-gen.; cytostatic; gene therapy;
 KW enzyme .
 XX OS Homo sapiens .
 XX PN WO200404196-A1 .
 XX PD 27-MAY-2004 .
 XX PF 05-NOV-2003; 2003WO-EPO12342 .
 XX PR 13-NOV-2002; 2002EP-00025502 .
 XX PA (PARB) BAYER HEALTHCARE AG .
 XX PI Golz S, Brueggemeier U, Summer H;
 XX DR WPI; 2004-440631/41 .
 XX PT Screening for therapeutic agents, useful in treating cardiovascular, reproductive, urological, hematological, respiratory system or cancer diseases, comprises contacting a test compound with a phosphodiesterase 7B .
 XX PS Disclosure: SEQ ID NO 2; 128PP; English .
 XX CC The present sequence is that of human phosphodiesterase 7B (PDE7B), an enzyme regulating intracellular levels of cAMP and cGMP. The invention relates to novel disease associations of PDE7B polynucleotides and polypeptides. It also relates to novel methods of screening for therapeutic agents for the treatment of cardiovascular diseases, disorders of the peripheral and central nervous system, reproduction diseases, urological diseases, haematological diseases, disorders of the respiratory system and cancer. PDE7B Polynucleotides, polypeptides and regulators or modulators of PDE7B activity (e.g. an RNA molecule, antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used in the treatment or diagnosis of these diseases and disorders .
 CC Sequence Match 92.9%; Score 1430; DB 8; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.8e-149;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Sequence Match 92.9%; Score 1430; DB 8; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.8e-149;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSCLMVERCGELLPEPDQNAKCVMLGDIRLRLGQTYVAERGSYPFTDFRLNISTYS	60	Db	1	MSCLMVERCGELLPEPDQNAKCVMLGDIRLRLGQTYVAERGSYPFTDFRLNISTYS	60
Qy	61	GEITGKCKKKRLLSFQRYFHASRLRGITIPQAPHLIDEDYLGQARHMLSKVGMWDIF	120	Db	1	MSCLMVERCGELLPEPDQNAKCVMLGDIRLRLGQTYVAERGSYPFTDFRLNISTYS	60
Qy	61	GEITGKCKKKRLLSFQRYFHASRLRGITIPQAPHLIDEDYLGQARHMLSKVGMWDIF	120	Db	61	GEITGKCKKKRLLSFQRYFHASRLRGITIPQAPHLIDEDYLGQARHMLSKVGMWDIF	120
Qy	121	LFDRLTNGSLVTLCLHNTGLHHPFLDMYTLHRFUMYQDYSQNPNTHNAHD	180	Db	61	GEITGKCKKKRLLSFQRYFHASRLRGITIPQAPHLIDEDYLGQARHMLSKVGMWDIF	120
Qy	121	LFDRLTNGSLVTLCLHNTGLHHPFLDMYTLHRFUMYQDYSQNPNTHNAHD	180	Db	121	LFDRLTNGSLVTLCLHNTGLHHPFLDMYTLHRFUMYQDYSQNPNTHNAHD	180
Qy	181	VTOQAMHCYKLEPKLASFPTPLDIMGLJAAAHDVDHPGVNQPLFLIKTNHHLANLYQNM	240	Db	121	LFDRLTNGSLVTLCLHNTGLHHPFLDMYTLHRFUMYQDYSQNPNTHNAHD	180
Qy	181	VTOQAMHCYKLEPKLASFPTPLDIMGLJAAAHDVDHPGVNQPLFLIKTNHHLANLYQNM	240	Db	181	VTOQAMHCYKLEPKLASFPTPLDIMGLJAAAHDVDHPGVNQPLFLIKTNHHLANLYQNM	240
Qy	241	VLENHHWRSTIGMRESRLLAHLPKEMT	268	Db	181	VTOQAMHCYKLEPKLASFPTPLDIMGLJAAAHDVDHPGVNQPLFLIKTNHHLANLYQNM	240
Qy	241	VLENHHWRSTIGMRESRLLAHLPKEMT	268	Db	181	VTOQAMHCYKLEPKLASFPTPLDIMGLJAAAHDVDHPGVNQPLFLIKTNHHLANLYQNM	240
Qy	241	VLENHHWRSTIGMRESRLLAHLPKEMT	268	Db	241	VLENHHWRSTIGMRESRLLAHLPKEMT	268

RESULT 6
 ADP79549 ;
 XX ID ADP79549 standard protein; 450 AA .
 AC ADP79549 ;
 XX DT 04-NOV-2004 (first entry)
 XX DB Human phosphodiesterase 7B nucleotide sequence .
 XX

RESULT 7
 AAY93567 ;
 ID AAY93567 standard; protein; 446 AA .
 AC AAY93567 ;
 XX

DT	25-SEP-2000	(first entry)	Qy	241 VLENHHWSTIGMRESRLAHLPKEMT	268
XX	Amino acid sequence of a murine phosphodiesterase enzyme.		Db	241 VLENHHWSTIGMRESRLAHLPKEMT	268
KW	Phosphodiesterase; PDE-XIV; murine; enzyme.				
XX	Mus sp.	RESULT 8			
PN	EP1018559-A1.	ID AAV93573 standard; protein; 445 AA.			
XX	AC AAV93573;	XX			
PD	12-JUL-2000.	AC			
XX	PP 09-NOV-1999; 99EPB-00308902.	XX	25-SEP-2000 (first entry)		
XX	PR 23-DEC-1998; 98GB-00028603.	XX	Amino acid sequence of a phosphodiesterase enzyme.		
PR 17-SEP-1999; 99GB-00022123.	XX	XX	KW Phosphodiesterase; PDE-XIV; enzyme.		
PA (PF12) PFIZER LTD.	XX	XX	OS Synthetic.		
PA (PF12) PFIZER INC.	XX	XX	FH Location/Qualifiers		
PI Fidock M.	XX	Key	Misc-difference 12		
XX	WPI: 2000-433274/38.	FT	Misc-difference 16		
DR N-PSDB; AAA46649.	XX	FT	Misc-difference 16		
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.	XX	FT	Misc-difference 18		
PT Disclosure; Page 39-41; 104pp; English.	XX	FT	Misc-difference 20..21		
PS	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).	XX	FT	/note= "these residues are a peptide comprising at least two or more of the above residues"	
CC Disclosure; Page 39-41; 104pp; English.	XX	FT	Misc-difference 30		
CC The present sequence represents a phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).	XX	FT	/note= "these residues are a peptide comprising at least two or more of the above residues"		
CC Sequence 446 AA;	XX	FT	Misc-difference 39		
CC Query Match 89.4%; Score 1376; DB 3; Length 446;	XX	FT	Misc-difference 56		
CC Best Local Similarity 95.1%; Pred. No. 2.7e-143;	XX	FT	Misc-difference 59		
CC Matches 255; Conservative 8; Mismatches 5; Indels 0; Gaps 0;	XX	FT	Misc-difference 114		
Qy 1 MSCLMVERCCEBILFPNPDQNAKCYCMLGIDRQLRGQTGVAAERRSYFPDFRLNNSTS 60	Db 1 MSCLMVERCCEBILFPNPDQNAKCYCMLGIDRQLRGQTGVAAERRSYFPDFRLNNSTS 60	FT	Misc-difference 141		
Qy 61 GEIGTKKKVRLISFLORYFHASRLIIRGLIPQAPHLIDDYLGAIRHMSKVETWDFDF 120	Db 61 GEIGTKKKVRLISFLORYFHASRLIIRGLIPQAPHLIDDYLGAIRHMSKVETWDFDF 120	FT	Misc-difference 168..169		
Db 121 LFDRLTNGSLVTLLCHLNTGHJLHFKLDMYTHRFLYMVOQDYHSQNPYRNHAAD 180	Qy 121 LFDRLTNGSLVTLLCHLNTGHJLHFKLDMYTHRFLYMVOQDYHSQNPYRNHAAD 180	FT	Misc-difference 391		
Db 121 LFDRLTNGSLVTLLCHLNTGHJLHFKLDMYTHRFLYMVOQDYHSQNPYRNHAAD 180	Db 121 LFDRLTNGSLVTLLCHLNTGHJLHFKLDMYTHRFLYMVOQDYHSQNPYRNHAAD 180	FT	Misc-difference 404		
Qy 181 VTQAMHCYKLPKLASFLPFLDPMGLLAAAHDVDHPVNVQPLIFTNHHLANLYQNS 240	Db 181 VTQAMHCYKLPKLASFLPFLDPMGLLAAAHDVDHPVNVQPLIFTNHHLANLYQNS 240	FT	Misc-difference 418..419		
Db 181 VTQAMHCYKLPKLASFLPFLDPMGLLAAAHDVDHPVNVQPLIFTNHHLANLYQNS 240	Qy 181 VTQAMHCYKLPKLASFLPFLDPMGLLAAAHDVDHPVNVQPLIFTNHHLANLYQNS 240	FT	Misc-difference 427..428		
		FT	/note= "these residues are a peptide comprising at least two or more of the above residues"		
		FT	Misc-difference 430		
		FT	/note= "these residues are a peptide comprising at least two or more of the above residues"		
		FT	Misc-difference 433..434		
		FT	/note= "these residues are a peptide comprising at least two or more of the above residues"		
		FT	Misc-difference 435..436		
		FT	/label= Gln, Gly, Thr, Pro, Ala		

FT PT Misc-difference /note= "these residues are a peptide comprising at least two or more of the above residues" 436; .137

FT PT Misc-difference /label= Ser, Glu, Thr, Leu /note= "these residues are a peptide comprising at least two or more of the above residues"

FT PT Misc-difference 440

FT PT Misc-difference 443; .144

FT PT Misc-difference 443; .144

FT PT /label= Asp, Ser, Ala, Thr /note= "these residues are a peptide comprising at least two or more of the above residues"

XX PN EP1018559-A1.

XX PD 12-JUL-2000.

XX PF 09-NOV-1999; 99EP-00308902.

XX PR 23-DEC-1999; 99GB-00028603.

PR 17-SEP-1999; 99GB-00022123.

XX PA (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

PI Fidock M;

XX WPI; 2000-433274/38.

DR XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

XX Disclosure; Page 64-66; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the Pbs-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of disorder associated with inappropriate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).

XX Sequence 445 AA;

SQ Query Match 88.1%; Score 1356; DB 3; Length 445; Best Local Similarity 95.1%; Pred. No. 4.56-141; Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MSCMLVERGEILPENPDNAKCVCMGLDIDRQGTYRAERGSPPRTDFRLLNSTYS 60

DB 1 GEIGTKKKVKRLISFQRYTHASRLLRGITIPOAHLIDEDYLGQAREMLSKYGMWDFDF 120

Qy 61 GEIGTKKKVKRLISFQRYTHASRLLRGITIPOAHLIDEDYLGQAREMLSKYGMWDFDF 120

DB 61 GEIGTKKKVKRLISFQRYTHASRLLRGITIPOAHLIDEDYLGQAREMLSKYGMWDFDF 120

Qy 121 LFDRLTNGNSLYTVLICHFLNTHGLIHHFKLDMYLTHRFUVMQDYHSQNPNPYHNAVAHD 180

DB 121 LFDRLTNGNSLYTVLICHFLNTHGLIHHFKLDMYLTHRFUVMQDYHSQNPNPYHNAVAHD 180

181 VTQAMHCYLKEPKLASEFTPLDIMGLIAAAAHDDHFGVNQPFLIKTNHHLANLYQNNMS 240

DB 181 VTQAMHCYLKEPKLASEFTPLDIMGLIAAAAHDDHFGVNQPFLIKTNHHLANLYQNNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

DB 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 9

AAV93574 standard; protein; 446 AA.

ID AAV93574

XX AC AAV93574;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of a phosphodiesterase enzyme.

XX KW Phosphodiesterase; PDE-XIV; enzyme.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT Misc-difference 12 /label= Val, Ile

FT Misc-difference 16 /label= Ser, Asn

FT Misc-difference 18 /label= Glu, Asp

FT Misc-difference 20 /label= Ser, Val, Asn, Ala

FT Misc-difference 21 /label= Ser, Val, Asn, Ala

FT Misc-difference 30 /label= Val, Ile

FT Misc-difference 39 /label= Pro, Arg

FT Misc-difference 56 /label= Asn, Ser

FT Misc-difference 59 /label= His, Tyr

FT Misc-difference 114 /label= Thr, Met

FT Misc-difference 141 /label= Ser, Thr

FT Misc-difference 168 /label= Glu, His, Ser, Gln

FT Misc-difference 169 /label= His, Tyr

FT Misc-difference 307 /label= Glu, His, Ser, Gln

FT Misc-difference 308 /label= Asp, Ala, Asn, Val

FT Misc-difference 350 /label= Asp, Ala, Asn, Val

FT Misc-difference 379 /label= Glu, Asp

FT Misc-difference 391 /label= Ser, Thr

FT Misc-difference 404 /label= His, Arg

FT Misc-difference 418 /label= Gly, Ser

FT Misc-difference 419 /label= Pro, Arg, Ser, Asn

FT Misc-difference 423 /label= Pro, Arg, Ser, Asn

FT Misc-difference 430 /label= His, Leu

FT Misc-difference 433 /label= Gin, Gly, Thr, Pro, Ala

FT	Misc-difference 434 /label= Gln, Gly, Thr, Pro, Ala	Db	121 LFDFRLTNGNSLVTLLCHLFNKGULIHFPLDMYTLHRLVMMQDYYXXNPYHNAVAHD 180
FT	Misc-difference 435 /label= Glu, Thr, Pro, Ala	Qy	181 VTQAMCYLKEPKLASFLLTLDMLGIIAAAADVDHAGCVNQPLIKITNWHHLANLYQNS 240
FT	Misc-difference 437 /label= Ser, Glu, Thr, Leu	Db	181 VTQAMCYLKEPKLASFLLTLDMLGIIAAAADVDHAGCVNQPLIKITNWHHLANLYQNS 240
FT	Misc-difference 438 /label= Ser, Glu, Thr, Leu	Qy	241 VLENHHWRSTIGMRESRLAHLPKEMT 268
FT	Misc-difference 441 /note= "optionally absent"	Db	241 VLENHHWRSTIGMRESRLAHLPKEMT 268
FT	Misc-difference 444 /label= Asp, Ser, Ala, Thr		
FT	Misc-difference 445 /label= Asp, Ser, Ala, Thr		
XX	EP1018559-A1.	RESULT 1.0	
XX	PD 12-JUL-2000.	ID AAY93575 standard; protein; 451 AA.	
XX	PF 09-NOV-1999; 99EP-00308902.	XX	
XX	PR 23-DBC-1998; 98GB-00028603.	AC AAY93575;	
XX	PR 17-SEP-1999; 99GB-00022123.	XX	25-SEP-2000 (first entry)
XX	(PF1Z) PFIZER LTD.	XX	Amino acid sequence of a phosphodiesterase enzyme.
PA	(PF1Z) PFIZER INC.	XX	KW Phosphodiesterase; PDE-XIV; enzyme.
XX	Key	XX	OS Synthetic.
PI	Fidock M;	XX	XX Location/Qualifiers
XX	WPI: 2000-433274/38.	FT	PH Misc-difference 12 /label= Val, Ile
XX	PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.	FT	PT Misc-difference 16 /label= Ser, Asn
PT	Disclosure; Page 70-72; 104pp; English.	FT	PT Misc-difference 18 /label= Glu, ASP
XX	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polypeptide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV expression and identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e., the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g., by enzyme linked immunosorbant assay (ELISA))	FT	PT Misc-difference 20 /label= Ser, Val, Asn, Ala
CC	Sequence 446 AA;	FT	PT Misc-difference 21 /label= Ser, Val, Asn, Ala
CC	SQ Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 24 /label= Val, Ile
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 26 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 28 /label= His, Arg
CC	SQ	FT	PT Misc-difference 30 /label= Glu, Asp
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 32 /label= Glu, Asp
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 34 /label= Ser, Thr
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 36 /label= His, Arg
CC	SQ	FT	PT Misc-difference 38 /label= Glu, Ser
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 40 /label= Glu, Ser
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 42 /label= Glu, Ser
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 44 /label= Pro, Arg, Ser, Asn
CC	SQ	FT	PT Misc-difference 46 /label= His, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 48 /label= Pro, Arg, Ser, Asn
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 50 /label= Pro, Arg, Ser, Asn
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 52 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 54 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 56 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 58 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 60 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 62 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 64 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 66 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 68 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 70 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 72 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 74 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 76 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 78 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 80 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 82 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 84 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 86 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 88 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 90 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 92 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 94 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 96 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 98 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 100 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 102 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 104 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 106 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 108 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 110 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 112 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 114 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 116 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 118 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 120 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 122 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 124 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 126 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 128 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 130 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 132 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 134 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 136 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 138 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 140 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 142 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 144 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 146 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 148 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 150 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 152 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 154 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 156 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 158 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 160 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 162 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 164 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 166 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 168 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 170 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 172 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 174 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 176 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 178 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 180 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 182 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 184 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 186 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 188 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 190 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 192 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 194 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 196 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 198 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 200 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 202 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 204 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 206 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 208 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 210 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 212 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 214 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 216 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 218 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 220 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 222 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 224 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 226 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 228 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 230 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 232 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 234 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 236 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 238 /label= Ser, Arg
CC	Query Match 88.1%; Score 1356; DB 3; Length 446;	FT	PT Misc-difference 240 /label= Ser, Arg
CC	Best Local Similarity 95.1%; Pred. No. 4.5e-141; Mismatches 0; Indels 0; Gaps 0;	FT	PT Misc-difference 242 /label= Ser, Arg
CC	Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	FT	PT Misc-difference 244 /label= Ser, Arg
CC	SQ	FT	PT Misc-difference 246 /label= Ser, Arg

FT	Misc-difference 438. .440 /note= "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"	Db	181 VTQAMHCYCLKEPKLASFLTPLDIMALGLAAAHHDVHDHPGVNQPFLIKTNHHLANLYONMS 240
FT	Misc-difference 442. .443 /note= "these residues are either Ser-Glu or Thr-Leu"	Qy	241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
FT	Misc-difference 446 /note= "optionally absent"	Db	241 VLENHHRSTIGMLRESRLLAHLPKEMT 268
FT	Misc-difference 449. .450 /note= "these residues are either Asp-Ser or Ala-Thr"		
XX		RESULT 11 AAV93572	
PN	EPI018559-A1.	ID	AAV93572 standard; protein; 437 AA.
XX		XX	
PD	12-JUL-2000.	AC	
XX		XX	
PF	09-NOV-1999; 99EPD-00308902.	DT	25-SEP-2000 (first entry)
XX		XX	
PR	23-DEC-1998; 98GB-00028603.	DE	Amino acid sequence of a phosphodiesterase enzyme.
PR	17-SEP-1999; 99GB-00022123.	KW	Phosphodiesterase; PDB-XIV; enzyme.
XX		XX	
PA	(PFTZ) PFIZER LTD.	OS	Synthetic.
PA	(PFTZ) PFIZER INC.	XX	
XX		XX	
PI	Fidock M;	FH	Key
XX		FT	Location/Qualifiers
WPI;	2000-433274/38.	FT	Misc-difference 12 /note= "any suitable peptide sequence or amino acid"
DR		FT	Misc-difference 16 /note= "any suitable peptide sequence or amino acid"
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.	FT	Misc-difference 18 /note= "any suitable peptide sequence or amino acid"
PT		FT	Misc-difference 20 /note= "any suitable peptide sequence or amino acid"
XX		FT	Misc-difference 29 /note= "any suitable peptide sequence or amino acid"
PS		FT	Misc-difference 38 /note= "any suitable peptide sequence or amino acid"
XX		FT	Misc-difference 55 /note= "any suitable peptide sequence or amino acid"
XX		FT	Misc-difference 58 /note= "any suitable peptide sequence or amino acid"
XX		FT	Misc-difference 113 /note= "any suitable peptide sequence or amino acid"
CC	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))	FT	Misc-difference 140 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 167 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 305 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 347 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 376 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 388 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 401 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 415 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 419 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 423 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 425 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 428 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 430 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 433 /note= "any suitable peptide sequence or amino acid"
CC		FT	Misc-difference 436 /note= "any suitable peptide sequence or amino acid"
XX	Sequence 451 AA;	XX	
SQ	Query Match Best Local Similarity 88.1%; Score 1356; DB 3; Length 451; Matches 255; Conservative 0; Mismatches 13; Indels 0; Gaps 0;		
Qy	1 MSCLMVERGEILPENPDNAKCVCMGIDIRLQGTGYRAERGSYPFDFRLLNSTYS 60	FT	
Db	1 MSCLMVERGEIXLPEXPQXXXCVCMLGDXRQLRGQTGXAEERGSYPFDFRLLNTYS 60	FT	
Qy	61 GEIGTKKKRKRLISFQRTFHASRLRGITPOAHLIDEDYIQAARMLSKYGMWDIDF 120	FT	
Db	61 GEIGTKKKRKRLISFQRTFHASRLRGITPOAHLIDEDYIQAARMLSKYGMWDIDF 120	FT	
Qy	121 LFDRLLTNGNSLVLICLHLFNTNGLIHHPKLDMTLHRLPVMQEDYHSQNPYHNAHAAD 180	FT	
Db	121 LFDRLLTNGNSLVLICLHLFNTNGLIHHPKLDMTLHRLPVMQEDYHSQNPYHNAHAAD 180	FT	
Qy	181 VTQAMHCYCLKEPKLASFLTPLDIMALGLAAAHHDVHDHPGVNQPFLIKTNHHLANLYONMS 240	PN	EP1018559-A1.

correlated with disease. HPDE, its fragments and antibodies specific for HPDE are useful as elements on a microarray which is useful to monitor or measure protein-protein interactions, drug-target interactions and gene expression profiles. This sequence represents HPDE-1

XX Sequence 502 AA;
Query Match Score 1280; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.5e-132; Indels 0; Gaps 0;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 GDIRLRGQTGVRERAERGSYSPIDFRLNNTYSGIGTKEKKVRLISFORYFHASRLLRG 87
Db 80 GDIRLRGQTGVRERAERGSYSPIDFRLNNTYSGIGTKEKKVRLISFORYFHASRLLRG 139

Qy 86 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 147
Db 140 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 199

Qy 148 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 207
Db 200 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 259

Qy 208 LAAAHDVDPHGUNQOPFLIKTNHHLANLYQNMSVLENHWRSTIGMLRSRLLAHLPKEM 267
Db 260 LAAAHDVDPHGUNQPFKLTKTNHHLANLYQNMSVLENHWRSTIGMLRSRLLAHLPKEM 319

Qy 268 T 268
Db 320 T 320

RESULT 15
ID ADJ58904 standard; protein; 502 AA.
XX ADJ58904;
XX DT 06-MAY-2004 (first entry)

XX Human cyclic nucleotide phosphodiesterase protein #1.
XX 27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer; cellular proliferation; cellular disorder; endothelial cell disorder; haematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; platelet disorder; gene therapy; human; cyclic; enzyme.
OS Homo sapiens.
XX US2004006016-A1.
XX 08-JAN-2004.
XX PF 11-MAR-2003; 2003US-00386414.

XX PR 11-TUN-1999; 99US-00310970.
PR 25-OCT-1999; 99US-00426282.
PR 16-MAY-2000; 2000US-00571189.
PR 22-SEP-2000; 2000US-00658266.
PR 28-NOV-2000; 2000US-00724599.
PR 07-DEC-2000; 2000US-0254037P.
PR 10-APR-2001; 2001US-0083082.
PR 16-MAY-2001; 2001US-00860193.
PR 31-OCT-2001; 2001US-0335044P.
PR 06-DEC-2001; 2001US-00010943.
PR 29-OCT-2002; 2002US-00283023.
XX PA (MILLI-) MILLENNIUM PHARM INC.

XX XX Kappeler-Libermann R, White D, Robison KE, Macbeth KJ, Carroll JM;

PI Cook WJ, Meyers RE, Chun M, Williamson MJ,

CC	XX	WPI: 2004-081738/08.
CC	DR	N-PDB; ADJ58903.
CC	PT	New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecules, useful for diagnosing or treating cancer, pain, or immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic and liver disorders.
SQ	XX	The present invention relates to an isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for diagnosing or treating cancer or aberrant cellular proliferation and/or differentiation, immune disorders, heart disorders, cardiovascular disorders including endothelial cell disorders, haematopoietic disorders, blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders and platelet disorders. The invention is also useful in gene therapy. The present sequence is human cyclic nucleotide phosphodiesterase.
	XX	Claim 4; SEQ ID NO 4; 245pp; English.
	PS	Sequence 502 AA;
	XX	Query Match Score 1280; DB 8; Length 502;
		Best Local Similarity 100.0%; Pred. No. 1.e-132;
		Mismatches 0; Indels 0; Gaps 0;
		Matches 241; Conservative 0;
	Qy	28 GDIRLRGQTGVRERAERGSYSPIDFRLNNTYSGIGTKEKKVRLISFORYFHASRLLRG 87
	Db	80 GDIRLRGQTGVRERAERGSYSPIDFRLNNTYSGIGTKEKKVRLISFORYFHASRLLRG 139
	Qy	86 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 147
	Db	140 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 199
	Qy	148 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 207
	Db	200 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 259
	Qy	208 LAAAHDVDPHGUNQOPFLIKTNHHLANLYQNMSVLENHWRSTIGMLRSRLLAHLPKEM 267
	Db	260 LAAAHDVDPHGUNQPFKLTKTNHHLANLYQNMSVLENHWRSTIGMLRSRLLAHLPKEM 319
	Qy	268 T 268
	Db	320 T 320
	Qy	88 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 147
	Db	140 IIPOQAPLHILDEDYLGQARMLSKYGMWDDIFIDRLNGSLVTLJCHLFNTHGLIH 199
	Qy	148 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 207
	Db	200 FKLDKVTYLHFLVMYQEDVHSQNPYTHAVAAADYQAMCYLKEPKLASFLTPIDMLGL 259
	Qy	208 LAAAHDVDPHGUNQOPFLIKTNHHLANLYQNMSVLENHWRSTIGMLRSRLLAHLPKEM 267
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	Db	320 T 320
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:57:15 ; Search time 19.9024 Seconds

(without alignments)
1392.313 Million cell updates/sec

Title: US-10-781-181-3

Perfect score: 15.10

Sequence: 1 MSCLMVERCGBILFFENPQN... GTWDDFIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

PIR_80;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query Match	Length	DB ID	Description
1	1430	92.9	450	2 JC7266	3', 5'-cyclic-nucle
2	907	58.9	498	2 A47286	3', 5'-cyclic-AMP P
3	331.5	21.5	584	2 B53109	3', 5'-cyclic-nucle
4	331.5	21.5	672	2 I61259	3', 5'-cyclic-nucle
5	320.5	21.5	673	2 I61358	3', 5'-cyclic-nucle
6	320.5	20.8	886	2 A54442	3', 5'-cyclic-nucle
7	317.5	20.6	562	2 I59143	CAMP phosphodiesterase
8	317.5	20.6	564	2 A40949	cyclic-AMP phospho
9	316.5	20.6	610	2 I67946	3', 5'-cyclic-nucle
10	316.5	20.6	844	2 I53865	phosphodiesterase
11	314.5	20.4	564	2 I61354	3', 5'-cyclic-nucle
12	314.5	20.4	736	2 I61355	phosphodiesterase
13	305	19.8	712	2 S71626	3', 5'-cyclic-nucle
14	301.5	19.6	323	2 S55348	3', 5'-cyclic-nucle
15	296.5	19.3	534	1 A44162	3', 5'-cyclic-nucle
16	296.5	19.3	535	1 A46378	3', 5'-cyclic-nucle
17	295.5	19.2	535	1 A44161	3', 5'-cyclic-nucle
18	295	19.2	536	2 I67945	3', 5'-cyclic-nucle
19	291	18.9	519	2 T14783	hypothetical prote
20	285	18.5	713	2 JW0088	3', 5'-cyclic-nucle
21	282.5	18.3	536	1 JC6129	3', 5'-cyclic-nucle
22	281	18.2	549	2 T16769	hypothetical prote
23	279	18.1	664	2 T24459	3', 5'-cyclic-nucle
24	278	18.1	530	1 A45334	hypothetical prote
25	269.5	17.5	659	2 JB0293	3', 5'-cyclic-nucle
26	269.5	17.5	885	2 JC7898	3', 5'-cyclic nucle
27	268	17.4	777	2 S65543	3', 5'-cyclic-nucle
28	263	17.1	768	2 T10796	3', 5'-cyclic-nucle
29	258	16.8	491	2 A40283	3', 5'-cyclic-nucle

RESULT 2
A47286
3', 5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000

RESULT 1

JC7266

3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human

N;Alternate names: cAMP-specific phosphodiesterase 7B

C;Species: Homo sapiens (man)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: JC7266

R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.

Biochem. Biophys. Res. Commun. 271, 575-583, 2000

A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.

A;Reference number: JC7266

A;Accession: JC7266

A;Gene: pde7B

A;Map position: 6q33-24

C;Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040

C;Experimental source: caudate nucleus

C;Genetics:

A;Keywords: phosphoric diester hydrolase

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase

C;Keywords: phosphoric diester hydrolase

C;Keywords: calmodulin-dependent, 3',5'

Query Match

92.9%; Score 1430;

DB 2;

Length 450;

Best Local Similarity

100.0%;

Pred. No. 8

2e-121;

Indels 0;

Gaps 0;

Matches 268;

Conservative 0;

Mi matches 0;

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 Db 218 KEKCKRPMQSISGVKLMISSLTNSCIPFGVKTQEODYHLAKE--LEDVNKGHLVER 274

Qy 122 FDRLTNGNSLVTLCH-LFNTGHLIHFCLDMVTLHFRFLMVQDHYHSQNPYTHAVHARD 180
 Db 275 IAEL-SGNRPLTVIMHTFOERDLKTFKIPVDTLITYMTLEDHYHADYHNTHAID 333

Qy 181 VTOAMHCYKKEPKLASLFTLDIMIGLLAAAHDYDHPGSYNQPELIKTNHHLANLYQMS 240
 Db 334 VVQSTHVLLSTPALEAVFTDLEILAIIFASAHDYDHPGSQNQLINTNSELALMYNDSS 393

Qy 241 VLENHHWRSTIGMIRE 255
 Db 394 VLENHHHLAVGFKLLOE 409

RESULT 5

161358 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human
 N;Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
 C;Accession: I61358; I38416
 R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993
 A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory gene
 A;Accession number: A54442; MUID:94019330; PMID:8413254

A;Cross-references: UNIPARC:UPI0000050EB5; GB:L20970; PID:NID:9347129; PID:AAA003592.1; PID:R;Brecker, P.; Oberholter, R.; Bach, C.; Yee, C.; Shelton, E.R.
 Gene 138, 253-256, 1994
 A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiesterase homologous to the duncle learning and memory gene
 A;Accession number: I38416; MUID:94171048; PMID:8125310

A;Molecule type: mRNA
 A;Residues: 1-673 <RES>

A;Cross-references: UNIPARC:UPI000016A067; EMBL:U028802; PID:NID:9433346; PID:AAU13745.1; PID:R;Genetics: GDB:PPB4D; PPDB3
 A;Gene: GDB:PPB4D; PPDB3
 A;Map position: 5q12-5q12
 A;Map position: 5q12-5q12
 C;Keywords: cAMP binding; phosphodiesterase homology <CNPD>
 F;432-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match Score 21.5%; Best Local Similarity 37.8%; Pred. No. 1.2e-21; Matches 74; Conservative.

Qy 66 KKVKVRLS---FORYFHASRLRGIIPOAPLHILDEDYLGQARHMLSKVGMNDFDIFL 121
 Db 218 KEKCKRPMQSISGVKLMISSLTNSCIPFGVKTQEODYHLAKE--LEDVNKGHLVER 274

Qy 122 FDRLTNGNSLVTLCH-LFNTGHLIHFCLDMVTLHFRFLMVQDHYHSQNPYTHAVHARD 180
 Db 275 IAEL-SGNRPLTVIMHTFOERDLKTFKIPVDTLITYMTLEDHYHADYHNTHAID 333

Qy 181 VTOAMHCYKKEPKLASLFTLDIMIGLLAAAHDYDHPGSYNQPELIKTNHHLANLYQMS 240
 Db 334 VVQSTHVLLSTPALEAVFTDLEILAIIFASAHDYDHPGSQNQLINTNSELALMYNDSS 393

Qy 241 VLENHHWRSTIGMIRE 255
 Db 394 VLENHHHLAVGFKLLOE 409

Qy 249 STIGMLRE 256
 Db 449 LATPDLDAVFTDLEILAIIFASAHDYDHPGSQNQLINTNSELALMYNDSS 508

Qy 249 STIGMLRE 256
 Db 509 VGFKLQE 516

RESULT 7

159143 cAMP phosphodiesterase - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: I59143
 R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.

C;Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAMP receptor
 A;Accession number: I59143; MUID:89264471; PMID:2542941

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-562 <RES>

RESULT 6

A54442 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice f

A;Cross-references: UNIPROT:P14646; UNIPARC:UPI00001440E1; GB:J04563; PIDN:9203967; PIDN:950096; C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent <CNP>; P;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent <CNP>;

Query Match 20.6%; Score 317.5; DB 2; Length 562; Best Local Similarity 34.1%; Pred. No. 1.4e-20; Matches 72; Conservative 43; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKCKYKRLIS---FORYPHASRURLRGITIQAQLHLLDDEYLQARHMLSKVGMWDFDIFL 121
Db 124 KCKKQQLMVIQSGYKLMISSSLNTTSRFGYNTENEHFLAKELEDINK--WGLNIFIN 180
Qy 122 FDRLTNGSLVTLCHLFNTHFLKMDMTLHRFLVMQDLYHSQSPYRNAAHADV 181
Db 181 VAGYSHNRPLTCIMYAIFQERDLIKTFKISSDTFVTTMFTLEDHYSDVAYNSLHAADV 242
Qy 122 FDRLTNGSLVTLCHLFNTHFLKMDMTLHRFLVMQDLYHSQSPYRNAAHADV 181
Db 182 TOAMHCYLUKEPKLASFLPTPLDIMALGLIAAAAHDYDHPGVNQPFLLIKTNHHLANLYQNMYSV 241
Db 243 AQSTHVLLSPLDAVFTDLEIILAAIFAAIHDPGVSNQPLINTNSEALMYNDES 302
Qy 242 LENHFWRTIGMLRESR -LLAHLPKENTGT 270
Db 303 LENHHLAVGFKLQLQEHCIDFQNLTKKQRQT 333

RESULT 9
I67946 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N:Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
N:Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, Splice Form 2 (cyclic AMP-spec.)
C:Species: Rattus norvegicus (Norway rat)
C:IDate: 29-May-1998 #Sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I67946; A32558; B32558
R:Boiger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes A. Reference number: I53865; PMID:95047482; PMID:958996
A:Accession: I67946
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: UNIPROT:P54748; UNIPARC:UPI000002A6D4; GB:L27062; NID:9436013; PIDN:4
R:Davis, R.L.; Takayasu, H.; Oberwine, M.; Myers, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A:Title: Cloning and characterization of mammalian homologs of the Drosophila duncane (+) gene
A:Reference number: A32558; PMID:89264472; PMID:2542942
A:Accession: A32558
A:Molecule type: mRNA
A:Residues: 1-598; T'/600-610 <DAV>
A:Cross-references: UNIPARC:UPI0000170937; GB:M26715; NID:9203982; PIDN:AAAC3769.1; PIDN:
A:Accession: B32558
A:Molecule type: mRNA
A:Residues: 26-598
A:Cross-references: UNIPARC:UPI0000170938; GB:M26716; NID:9203984; PIDN:AA41101.1; PIDN:
A:Accession: C32558
A:Molecule type: mRNA
A:Residues: 85-120-154-598 'T' 600-610 <DA2>
A:Cross-references: UNIPARC:UPI0000170939; GB:M26717; NID:9203986;
A:Note: Splice Form RD3
C:Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;14-20/Region: responsible for membrane association
P:26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pre
F:85-120-154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #st
P:184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 20.6%; Score 316.5; DB 2; Length 610;
Best Local Similarity 33.2%; Pred. No. 1.9e-20;
Matches 71; Conservative 32; Mismatches 86; Indels 25; Gaps 2;

Qy 43 RGSYPFDPLRLNSTSGEITKKVKRLLSFQRYFHASRLLRGIIHQAPHLLDDEDYL 102
Db 80 RQSQPNSQITGKKLWHTGSLNNT-----VPRFGVKTQDQEDLL 117
Qy 103 GOARHMLSKVGMWDFDIFLFLFDRLTLNGNSLVTLLCHLFTNTHGLJHFKLDMVTLHRLFLMV 162

Query Match 20.6%; Score 317.5; DB 2; Length 564;

Db 118 AQBLENLSSK--WGLNIFCVSYAGGRSISCLIMTYIFQERDLKKFHTFVDTMMYMLTL 174
 Qy 163 QEDYHSQNQPHNAVHAADYTOAMHCYLKEPKLASFLPTDIMLGLLAATAAHVDYDHPGYNQ 222
 Db 175 EDHYHADYAVHNSSLAADYDQSTHVLATPALDAVFTDLEILALFAARAHVDHPGVSN 234
 Qy 223 PFLIKTNHHHLANLYQNMVSILENNHWRSTGMLRE 256
 Db 235 QFLINTNSELALMNTDESTELENHLLAVGFKLQLQE 268

RESULT 10

153865 phosphodiesterase - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 153865
 R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
 Gene 149, 237-244, 1994
 A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
 A;Reference number: 153865; MUID:95047482; PMID:7958996
 A;Accession: 153865
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:P54748; UNIPARC:UPI0000127BF5; GB:L27057; NID:g31334904; PIDN:F; 418-646/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.6%; Score 316.5; DB 2; Length 844;
 Best Local Similarity 33.2%; Pred. No. 2.9e-20;
 Matches 71; Conservative 32; Mismatches 86; Indels 25; Gaps 2;

Qy 43 RGSYPPFDRLINSTTYSGEIGTKKKVVRLLSPQRYFAASRLLRGGIIPQAPLHLDDEYL 102
 Db 3114 RQSQEMSQITGLKLUVHTSGLNTN-----VPRFGVKTIDQEDL 351

Qy 103 QGARHMLSKVGMDPFDIFPDRLLTNGNSLYTLLCHLNFNTHGLIHFKUDMVTLLHRFLWN 162
 Db 352 AQELENLSK--WGLNIFCVSEYAGGRSISCLIMTYIFQERDLKKFHTFVDTMMYMLTL 408

Qy 163 QEDYHSQNQPHNAVHAADYTOAMHCYLKEPKLASFLPTDIMLGLLAATAAHVDYDHPGYNQ 222
 Db 409 EDHYHADYAVHNSSLAADYDQSTHVLATPALDAVFTDLEILALFAARAHVDHPGVSN 468

Qy 223 PFLIKTNHHHLANLYQNMVSILENNHWRSTGMLRE 256
 Db 469 QFLINTNSELALMNTDESTELENHLLAVGFKLQLQE 502

RESULT 11

JC5159 3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBPI06) -
 C;Species: Homo sapiens (man)
 C;Accession: JC1519; MUID:93314968; PMID:83920015
 R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, R
 Gene 129, 239-247, 1993
 A;Reference number: JC1519; MUID:93314968; PMID:83920015
 A;Accession: JC1519
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014C5AB; GB:L12686
 A;Residues: 1-564 <OBE>
 A;Experimental source: lymphocyte
 A;Note: only partial nucleotide sequence is given
 R;McLaughlin, M.M.; Cieplinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.; ...
 J. Biol. Chem. 268, 6470-6476, 1993
 A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.
 f mRNA.
 A;Accession number: A45500; MUID:93203241; PMID:8384210
 A;Molecule type: mRNA
 A;Residues: 1-564 <MCU>

Db 118 AQBLENLSSK--WGLNIFCVSYAGGRSISCLIMTYIFQERDLKKFHTFVDTMMYMLTL 174
 Qy 163 QEDYHSQNQPHNAVHAADYTOAMHCYLKEPKLASFLPTDIMLGLLAATAAHVDYDHPGYNQ 222
 Db 175 EDHYHADYAVHNSSLAADYDQSTHVLATPALDAVFTDLEILALFAARAHVDHPGVSN 234
 Qy 223 PFLIKTNHHHLANLYQNMVSILENNHWRSTGMLRE 256
 Db 235 QFLINTNSELALMNTDESTELENHLLAVGFKLQLQE 268

A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:929387; PIDN:AAA36426.1; PIDN:AAA36426.2
 A;Experimental source: frontal cortex
 A;Sequence extracted from NCBI backbone (NCBIN:127929, NCBIPI:127930)
 A;Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBIPI:127930)
 R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.
 Mol. Cell. Biol. 13, 6558-6571, 1993
 A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory
 A;Reference number: A54442; MUID:94019330; PMID:8413254
 A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-564 <RES>
 A;Cross-references: UNIPARC:UPI000014C5AB; GB:L20971; PIDN:AAA03593.1; PIDN:AAA03593.2
 C;Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'-
 C;Keywords: Phosphodiesterase homology <CNP>
 F;233-461/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 20.4%; Score 314.5; DB 2; Length 564;
 Best Local Similarity 33.6%; Pred. No. 2.6e-20;
 Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKVKVKLRS---FQRYFHASRLRGGIIPQAPLHLDDEYLQGARHMLSKVGMDDFPL 121
 Db 126 KKCKQQLMTQISGVKLMKHSSSLNTNTSREGNTNTEDHLAKELDINK--WGLNIFN 182

Query Match 20.4%; Score 314.5; DB 2; Length 564;
 Best Local Similarity 33.6%; Pred. No. 2.6e-20;
 Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 122 FDRLTNGNSLVTLLCHLPNTNGLIHFKUDMVTLLHRFLVMQDYSHSNPNYHSAVHADY 181
 Db 183 VAGYSHNRPLTCIMYAIFQERDLKLTFRISSTDFITMMTLEHYHSDVAYNSLHADY 242

Qy 182 TOAMHCYLKEPKLASFLTPLDIMLGLLAAAHVDYDHPGVNOPLFLKTNHHLANLYQNMVS 241
 Db 243 AQSTHVLLSTPAIDAVFTDLEIAAFAAAIHVDHPGVSNQFLINTNSELALMYNDESV 302

Qy 242 LENHWRSTGMLRESR -LLAHLPKEMTGT 270
 Db 303 LENHHLAVGFKLQEEHDIFMNLTKQRQT 333

RESULT 12

161354 phosphodiesterase - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C;Accession: 161354
 R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.
 Mol. Cell. Biol. 13, 6558-6571, 1993
 A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory
 A;Reference number: A54442; MUID:94019330; PMID:8413254
 A;Accession: 161354
 A;Molecule type: mRNA
 A;Residues: 1-736 <RES>

Qy 66 KKVKVKLRS---FQRYFHASRLRGGIIPQAPLHLDDEYLQGARHMLSKVGMDDFPL 121
 Db 298 KKCKQQLMTQISGVKLMKHSSSLNTNTSREGNTNTEDHLAKELDINK--WGLNIFN 354

Query Match 20.4%; Score 314.5; DB 2; Length 736;
 Best Local Similarity 33.6%; Pred. No. 3.6e-20;
 Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 122 FDRLTNGNSLVTLLCHLPNTNGLIHFKUDMVTLLHRFLVMQDYSHSNPNYHSAVHADY 181
 Db 355 VAGYSHNRPLTCIMYAIFQERDLKLTFRISSTDFITMMTLEHYHSDVAYNSLHADY 414

Qy 182 TOAMHCYLKEPKLASFLTPLDIMLGLLAAAHVDYDHPGVNOPLFLKTNHHLANLYQNMVS 241
 Db 415 AQSTHVLLSTPAIDAVFTDLEIAAFAAAIHVDHPGVSNQFLINTNSELALMYNDESV 474

Qy 242 LENHWRSTGMLRESR -LLAHLPKEMTGT 270

Search completed: March 10, 2006, 20:03:02
Job time : 22.9024 secs

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Total number of hits satisfying chosen parameters:	2166443
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0‡ Maximum Match 100‡ Listing first 45 summaries
Database :	UniProt 05.80;* 1: uniprot_sprot;* 2: uniprot_trembl;*
Scoring table:	BLOSUM62
Run on:	March 10, 2006, 19:52:25 ; Search time 120.195 Seconds (without alignments) 1690.519 Million cell updates/sec
Title:	US-10-781-181-3
Perfect score:	1540
Sequence:	1 MSCLMYVERCGBILFENPQDN.....GTWDFDFIFLFDRLTNGNSLV 288
ALIGNMENTS	
RESULT 1	
PDB ID:	PDB7B_HUMAN
ID:	Q9NFS6;
AC:	AC
STANDARD:	PRT;
PRIT:	450 AA.
DT:	16-OCT-2001 (Rel. 40, Created)
DT:	16-OCT-2001 (Rel. 40, Last sequence update)
DT:	10-MAY-2005 (Rel. 47, Last annotation update)
DE:	CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN:	Name=PDB7B;
OS:	Home sapiens (Human).
OC:	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC:	NCBI_TaxID=9606;
RN:	RP
RP:	NUCLEOTIDE SEQUENCE.
RC:	RC TISSUE=Brain
RX:	MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;
RA:	Sasaki T., Kotera J., Yuasa K., Omori K.;
RT:	"Identification of human PDB7B, a cAMP-specific phosphodiesterase."
RL:	Biochem. Biophys. Res. Commun. 271:575-583 (2000).
RN:	[2]
RP:	NUCLEOTIDE SEQUENCE.
RC:	RC TISSUE=Brain
RX:	MEDLINE=0329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
RA:	Gardner C.E., Robos N.M., Cawkill D., Fidock M.D.;
RT:	"Cloning and characterisation of the human and mouse PDB7B, a novel CAMP-specific nucleotide phosphodiesterase."
RL:	Biochem. Biophys. Res. Commun. 272:186-192 (2000).
RN:	[3]
RP:	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC:	RC TISSUE=Brain
RX:	MEDLINE=22388057; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA:	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Gardner C.E., Robos N.M., Cawkill D., Fidock M.D.;
RA:	Klausner R.D., Collins F.S., Wagner L., Shenm C.M., Schuller G.D., Altchul S.F., Zesberg B., Buetow K., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Fahy J., Hilton B., Soares M.B., Donaldson T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bobk S.A., McEwan P.J., McKernan K.J., Malek J.A., Garcia A.M., Hale S., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiteing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA: Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalack U., Smalius D.E., Schnurch A., Schein J.B., Jones S.J.M., Marrs M.A.;
RA:	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT:	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL:	-1- FUNCTION: May be involved in the control of cAMP-mediated neural
CC:	

CC activity and cAMP metabolism in the brain.
 CC -I CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -I COFACTOR: Divalent cations (By similarity).
 CC -I ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
 CC -I Insensitive to zaprinast, rolopram, and milrinone.
 CC -I PATHWAY: Cyclic nucleotide metabolism.
 CC -I TISSUE SPECIFICITY: Highly expressed in brain. Also expressed in heart, liver, skeletal muscle and pancreas.
 CC -I DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.
 CC -I SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC DR AP038040; BA96537; 1; mRNA.
 CC DR EMBL; A2251860; CB92441; 1; mRNA.
 CC DR EMBL; B0275032; ARH75083; 1; mRNA.
 CC DR EMBL; B0275033; ARH75083; 1; mRNA.
 CC PTR; JC7266; JC7266.
 CC DR PDB; 1LKW; Model: A=104-433.
 CC DR Ensemble; ENSG0000171408; Homo sapiens.
 CC DR HGNC; HGNC:8792; PDE7B.
 CC DR MIM; 60445; .
 CC DR GO; GO:0004115; P:cAMP-specific phosphodiesterase activity; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR GO; GO:007268; P:synaptic transmission; TAS.
 CC DR InterPro; IPR002033; PDBase_I; 1.
 CC DR Pfam; PF00233; PDBase_I; 1.
 CC DR PRINTS; PR00387; EDIESTERASE1.
 CC DR PROSITE; PS00126; PDEASE_I; 1.
 CC DR 3D-STRUCTURE; CAMP; Hydrolase.
 CC KW REGION_172 MW; Catalytic (By similarity).
 SQ SEQUENCE 450 AA; BCI42F3E2BD0028 CRC64;

Query Match 92.9%; Score 1430; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 5..8e-122;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSCLMVERGEGELPENPDQNAKCVCMGLGDIRURGQTGVRAERGSYPIDFILLNSTYS 60
 Db 1 MSCLMVERGEGELPENPDQNAKCVCMGLGDIRURGQTGVRAERGSYPIDFILLNSTYS 60
 Qy 1 61 GEIGTICKKKVRLISFQRYFHASRLLRGITIPQAPLHLDDEDYLGQARMLSKVGMWDFDF 120
 Db 61 GEIGTICKKKVRLISFQRYFHASRLLRGITIPQAPLHLDDEDYLGQARMLSKVGMWDFDF 120
 Qy 121 LFDRLTNGNSLYLVLCHLFLENTHGLIHFKLDMVTLRFLVMQEDYHSQNPFYHNAHAAD 180
 Db 121 LFDRLTNGNSLYLVLCHLFLENTHGLIHFKLDMVTLRFLVMQEDYHSQNPFYHNAHAAD 180
 Qy 181 VTOQAMHCYTKLEPKLASFLTPLDIMLGLIAAAAHVDIFGVNQPLFLKTNHHHLANLYQNM 240
 Db 181 VTOQAMHCYTKLEPKLASFLTPLDIMLGLIAAAAHVDIFGVNQPLFLKTNHHHLANLYQNM 240
 Qy 241 VLENHHWRSTIGMRESRLAHLPKEMT 268
 Db 241 VLENHHWRSTIGMRESRLAHLPKEMT 268

RESULT 2
 Q5VWY9 HUMAN PRELIMINARY; PRT; 450 AA.
 ID Q5VWY9_HUMAN PRELIMINARY;
 AC Q5VWY9;
 DT 01-FEB-2005 (TREMBLre1. 29, Created)
 DT 13-SEP-2005 (TREMBLre1. 29, Last sequence update)
 DT 10-MAY-2005 (TREMBLre1. 31, Last annotation update)

OTTHUHMP00000017267.

GN Name=PDB7B; ORFNames=RP11-472B5.2-001;
 OS Homo sapiens (Human).
 OC Fukuyora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OX NCBI_TAXID=9606;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RA Thomas D.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 RN [2].
 RP NUCLEOTIDE SEQUENCE.
 RA Williams S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 RN [3].
 RP NUCLEOTIDE SEQUENCE.
 RA Cobley V.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL360178; CAH73075; 1; Genomic_DNA.
 DR EMBL; AL133319; CAH73075; 1; Genomic_DNA.
 DR EMBL; AL133319; CAH73075; 1; Genomic_DNA.
 DR EMBL; AL133319; CAH73075; 1; JOINED; Genomic_DNA.
 DR EMBL; AL133319; CAH73075; 1; JOINED; Genomic_DNA.
 DR EMBL; AL133319; CAH73332; 1; JOINED; Genomic_DNA.
 DR GO; GO:0003824; F:cyclic-nucleotide phosphodiesterase activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR002073; PDBase_I; 1.
 DR InterPro; IPR002073; PDBase_I; 1.
 DR Pfam; PF00233; PDBase_I; 1.
 DR PRINTS; PR00387; EDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 SQ SEQUENCE 450 AA; BCI42F3E2BD0028 CRC64;

Query Match 92.9%; Score 1430; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 5..8e-122; Mismatches 0; Indels 0; Gaps 0;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSCLMVERGEGELPENPDQNAKCVCMGLGDIRURGQTGVRAERGSYPIDFILLNSTYS 60
 Db 1 MSCLMVERGEGELPENPDQNAKCVCMGLGDIRURGQTGVRAERGSYPIDFILLNSTYS 60
 Qy 61 GEIGTICKKKVRLISFQRYFHASRLLRGITIPQAPLHLDDEDYLGQARMLSKVGMWDFDF 120
 Db 61 GEIGTICKKKVRLISFQRYFHASRLLRGITIPQAPLHLDDEDYLGQARMLSKVGMWDFDF 120
 Qy 121 LFDRLTNGNSLYLVLCHLFLENTHGLIHFKLDMVTLRFLVMQEDYHSQNPFYHNAHAAD 180
 Db 121 LFDRLTNGNSLYLVLCHLFLENTHGLIHFKLDMVTLRFLVMQEDYHSQNPFYHNAHAAD 180
 Qy 181 VTOQAMHCYTKLEPKLASFLTPLDIMLGLIAAAAHVDIFGVNQPLFLKTNHHHLANLYQNM 240
 Db 181 VTOQAMHCYTKLEPKLASFLTPLDIMLGLIAAAAHVDIFGVNQPLFLKTNHHHLANLYQNM 240
 Qy 241 VLENHHWRSTIGMRESRLAHLPKEMT 268
 Db 241 VLENHHWRSTIGMRESRLAHLPKEMT 268

RESULT 3
 PDB7B MOUSE
 ID PDB7B MOUSE STANDARD; PRT; 446 AA.
 AC Q9QXQ;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-Oct-2005 (Rel. 40, Last sequence update)
 DT 10-May-2005 (Rel. 47, Last annotation update)
 DE CAMP-Specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
 GN Name=Pde7b;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;
 OC Muroidea; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20087273; PubMed=10618442; DOI=10.1073/pnas.97.1.472;
 RA Herman J.M., Soderling S.H., Glaves N.A., Beavo J.A.;
 RT "Cloning and characterization of PDE7B, a cAMP-specific
 phosphodiesterase";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:472-476 (2000).
 RN [2]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J;
 MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
 RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
 RT "Cloning and characterisation of the human and mouse PDE7B, a novel
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 CC -!- FUNCTION: May be involved in the control of cAMP-mediated neural
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 CC -!- COFACTOR: Divalent cations (By similarity).
 CC -!- ENZYME REGULATION: Inhibited by dipyradomole, IBMX and SCH51866.
 CC -!- INSENSITIVE TO zappinast, rolipram, and milrinone.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain.
 CC -!- DOMAIN: Composed of C-terminal catalytic domain containing two
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 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
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 CC -----
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FT REGION 172 Catalog (By similarity).
 SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;

Query Match 89.4%; Score 1376; DB 1; Length 446;
 Best Local Similarity 95.1%; Pred. No. 5e-117; Mismatches 8; Indels 0; Gaps 0;
 Matches 255; Conservative 1.
 Db 1 MSCLMVERGBILPENPDONAKCVCMLGDTLRLCGTGAERGSYPFDFLRLNSTTYS 60
 1 MSCLMVERGBILPENPDONAKCVCMLGDTLRLCGTGAERGSYPFDFLRLNNNTS 60
 Qy 61 GEIGTKKKKTKRLLSFRQYTHASRLRGITPQAPHLIDEDYLQARHMSKVGMWDFDIF 120
 Db 61 GEIGTKKKKTKRLLSFRQYTHASRLRGITPQAPHLIDEDYLQARHMSKVGMWDFDIF 120
 Qy 121 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYHSNPYNAVHAAD 180
 1 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYGHNPYNAVHAAD 180
 Db 121 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYGHNPYNAVHAAD 180
 Qy 181 VTOAMHCYKKEPKLASFLTPDLMGLLAAAHDVDHPGYNOPPLIKTNHHLANLYQNM 240
 Db 181 VTOAMHCYKKEPKLASFLTPDLMGLLAAAHDVDHPGYNOPPLIKTNHHLANLYQNM 240

Qy 241 VLENHHRSTIGMLRESRLAHLPKEMT 268
 OC Mus musculus (Mouse).
 NCBI_TaxID=10090;
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 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Urinary bladder; DE enriched library, clone:9530027016 product: phosphodiesterase 7B, full
 MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
 RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
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DR AF190639; AF2251859; CAB92530.1; mRNA.
 DR HSSMBP; Q8499; LOIN; mRNA.
 DR Ensembl; ENSMUSG00000019990; Mus musculus.
 DR MGI; MGI:1352252; Pde7b.
 DR GO:0004115; F:AMP-specific phosphodiesterase activity; IDA.
 DR InterPro; IPR002073; PDBase.
 DR Pfam; PF00233; PDBase; J, 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR PROSITE; PS00126; PDEASE_I; 1.
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 Db 1 MSCLMVERGBILPENPDONAKCVCMLGDTLRLCGTGAERGSYPFDFLRLNSTTYS 60
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 Qy 181 VTOAMHCYKKEPKLASFLTPDLMGLLAAAHDVDHPGYNOPPLIKTNHHLANLYQNM 240
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Qy 241 VLENHHRSTIGMLRESRLAHLPKEMT 268
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 DR Pfam; PF00233; PDBase; J, 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 DR CAMP; Hydrolase.
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 Db 1 MSCLMVERGBILPENPDONAKCVCMLGDTLRLCGTGAERGSYPFDFLRLNSTTYS 60
 1 MSCLMVERGBILPENPDONAKCVCMLGDTLRLCGTGAERGSYPFDFLRLNNNTS 60
 Qy 61 GEIGTKKKKTKRLLSFRQYTHASRLRGITPQAPHLIDEDYLQARHMSKVGMWDFDIF 120
 Db 61 GEIGTKKKKTKRLLSFRQYTHASRLRGITPQAPHLIDEDYLQARHMSKVGMWDFDIF 120
 Qy 121 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYHSNPYNAVHAAD 180
 1 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYGHNPYNAVHAAD 180
 Db 121 LFDRLTNGSLVTLCHLNTHGLIHHFLCDMVLTHRFLYMQEDYGHNPYNAVHAAD 180
 Qy 181 VTOAMHCYKKEPKLASFLTPDLMGLLAAAHDVDHPGYNOPPLIKTNHHLANLYQNM 240
 Db 181 VTOAMHCYKKEPKLASFLTPDLMGLLAAAHDVDHPGYNOPPLIKTNHHLANLYQNM 240

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA Shibata K., Ichii M., Aizawa K., Nagabuchi S., Sasaki N., Carninci P.,	OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Itoh M.,	OC Muridae; Murinae; Rattus.
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M.,	NCBI_TAXID=10116;
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashihagi K.,	RN
RA Fujiwara S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watanuki M.,	RP NUCLEOTIDE SEQUENCE.
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuo S., Kawai J.,	RC TISSUE=Brain;
RA Okada Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,	RA Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";	RL EMBL; AB057409; BAB79637.1.; mRNA.
RT [6]	DR Ensembl; ENSG0000013436; Rattus norvegicus.
RN	DR SGD; 621016; Pde7b.
RP NUCLEOTIDE SEQUENCE.	DR GO; GO:004114; F; 3'-cyclic-nucleotide phosphodiesterase activity; IEA.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;	DR GO; GO:0016787; F; hydrolase activity; IEA.
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	DR GO; GO:0007165; P; signal transduction; IEA.
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	DR InterPro; IPR03607; Met_phos_hydro.
RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,	DR InterPro; IPR02073; PDEase.
RA Hori F., Imotani K., Iishi Y., Ichio M., Kasukawa T.,	DR Pfam; PF00233; PDEase_I_1.
RA Karoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	DR SMART; PR00387; PDESTERASE1.
RA Kuribara C., Matsuyaki T., Miyazaki A., Murata M., Nakamura M.,	DR SMART; SM00471; Hdc1.
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.
RA Saitoh R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sanoo H.,	KW Hydrolase.
RA Tagawa A., Shibusawa A., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,	SQ SEQUENCE 446 AA; 51475 MW; 01567BDABC905D19 CRC64;
RA Tonaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,	Best Local Similarity 94.0%; Pred. No. 3.e-116;
RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	Matches 252; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
DR EMBL; AY03585; Bac29052.1.; mRNA.	QY 1 MSCLMVERGEELIFENPDONAACKVCMGLDIRLRGQTGYRAERRGSYPFTDFRLNSTTYS 60
DR MG1; MG1:135275; Pde7b.	Db 1 MSCLMVERGEELIFENPDONAACKVCMGLDIRLRGQTGYRAERRGSYPFTDFRLNSTTYS 60
DR GO; GO:004115; P; cAMP-specific phosphodiesterase activity; IDA.	QY 61 GEIGTKKKVKKRLLSFLQQYFHAASRLLRGQTGYRAERRGSYPFTDFRLNSTTYS 60
DR InterPro; IPR003607; Met_phos_hydro.	Db 61 GEIGSKKKVKKRLLSFLQRHESRLLRGQTGYRAERRGSYPFTDFRLNSTTYS 60
DR Pfam; PF00233; PDEase_I_1.	Db 121 LFDRLTNGSLVTLCHLFNTCLHFKLDMVTLHRLPVMQEDYHNPYNAVHAD 180
DR PRINTS; PR00387; EDIBESTERASE1.	DR 121 LFDRLTNGSLVTLCHLFNTCLHFKLDMVTLHRLPVMQEDYHNPYNAVHAD 180
DR SMART; SM00471; Hdc1.	DR 61 VTOAMHCYLKEPLKASFLTPDLMGLLAAAHHDVHFGVNQFLIKTNHHLANLYQMS 240
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 181 VTOAMHCYLKEPLKASFLTPDLMGLLAAAHHDVHFGVNQFLIKTNHHLANLYQMS 240
DR Pftan; PR00233; PDEase_I.	QY 121 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 181 VTOAMHCYLKEPLKASFLTPDLMGLLAAAHHDVHFGVNQFLIKTNHHLANLYQMS 240
DR SMART; SM00471; Hdc1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	QY 121 LFDRLTNGSLVTLCHLFNTCLHFKLDMVTLHRLPVMQEDYHNPYNAVHAD 180
DR Pftan; PR00233; PDEase_I.	Db 121 LFDRLTNGSLVTLCHLFNTCLHFKLDMVTLHRLPVMQEDYHNPYNAVHAD 180
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DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	QY 61 GEIGTKKKVKKRLLSFLQQYFHAASRLLRGQTGYRAERRGSYPFTDFRLNSTTYS 60
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DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
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DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
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DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
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DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR SMART; SM00471; Hdc1.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PROSITE; PS00126; PDESE_I; UNKNOWN_1.	Db 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR Pftan; PR00233; PDEase_I.	QY 241 VLENHHHRSTGMLRESRLLAHLPKENT 268
DR PRINTS; PR00387; EDIBESTERASE1.	Db 241 VLENHHHRST

GO; GO:004114; F:3',5'-cyclic-nucleotide phosphodiesterase a... . ; IFA.	Db	224 IIPQAPLHLDDELYGQARHMLSKYGMWDFDIFLFLFDRLTNNSLYLTLCLHFNTGLIHH 283
GO; GO:0016787; F:hydrolase activity; IFA.	Qy	148 PKLDMVTLHRLFLVNQEDYHSQNPKYHNAHAADTVQAMHCKYLKEPKLASFTPLDMLGL 207
DR IntersPro: IPR03607; P:signal transduction; IFA.	Db	284 PKLDMVTLHRLFLVNQEDYHSQNPKYHNAHAADTVQAMHCKYLKEPKLASFTPLDMLGL 343
DR InterPro: IPR02073; PDBase.	Qy	208 LAAAHADYDHPGVNQPFLIKTNHHLANLYNQMSVLHENHWSTIGMLRESRLLAHLPKEM 267
DR PRINTS; PF0233; PDBase I ; I.	Db	344 LAAAHADYDHPGVNQPFLIKTNHHLANLYNQMSVLHENHWSTIGMLRESRLLAHLPKEM 403
SMART; SMD0471; HDG_C_1.	Qy	SEQUENCE 459 AA; 52680 MW; A3F26E95C7FC00A5 CRC64;
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.	Db	268 T 268
KW hydroxylase.	Qy	Query Match Score 1350.5; DB 2; Length 459;
Best Local Similarity 89.7%; Pred No. 1.e-114;	Db	404 T 404
Matches 255; Conservative 10; Mismatches 6; Indels 13; Gaps 1;	Qy	RESULT 8 Q4RR95_TETNG
1 MSCLMVERCSEILFENPDONAKCVML-----CDIRLNGQTGYRAERRGSYP 47	AC	Q4RR95_TETNG PRELIMINARY; PRT; 456 AA.
1 MSCLMVERCSEILFENPDONAKCVMLAASSPPPLPMAGQDPVRLRGQTGYPAERGSYP 60	AC	Q4RR95_TETNG PRELIMINARY; PRT; 456 AA.
48 FIDFRLLNNTSYSGEGTKKVKRLLSFQYSSFRASRLLRGITIOPAHLILBDYLGQARI 107	DT	13-SEP-2005 (TREMBLrel. 31, Created)
61 FIDFRLLNNTSYSGEGSKKVKRLLSFQYSSFRASRLLRGITIOPAHLILBDYLGQARI 120	DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)
61 Chromosome 14 SCAF15003, whole genome shotgun sequence.	DB	13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE (Fragment).	DN	ORFNAME=GSP1ENG00030267001;
GN Tetradoon nigroviridis (Green puffer).	OS	Tetradoon nigroviridis
Qy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetradontoiidea; Tetraodontidae; Tetraodon.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetradontoiidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=9983;	OX	NCBI_TaxID=9983;
RN RP NUCLEOTIDE SEQUENCE.	RA	Jailion O., Autry J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Basilia C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vachal M., Biemont C., Skalli Z., Cattolico L., Poulaen J., De Berardinis V., Raoult C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volkoff J.N., Guigo R., Zody M.C., Mesirow J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn M., Robinson-Rechavi M., Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C., Wincker P., Landre B.S., Weissenbach J., Roest Crollius H., RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; RT Nature 431:946-957 (2004). RN [2]
Qy 228 TNHHHLANLYNQMSVLHENHWSTIGMLRESRLLAHLPKEMT 268	RA	Jailion O., Autry J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Basilia C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vachal M., Biemont C., Skalli Z., Cattolico L., Poulaen J., De Berardinis V., Raoult C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volkoff J.N., Guigo R., Zody M.C., Mesirow J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn M., Robinson-Rechavi M., Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C., Wincker P., Landre B.S., Weissenbach J., Roest Crollius H., RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; RT Nature 431:946-957 (2004). RN [2]
Db 241 TNHHHLANLYNQMSVLHENHWSTIGMLRESRLLAHLPKEMT 281	RA	Jailion O., Autry J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Basilia C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vachal M., Biemont C., Skalli Z., Cattolico L., Poulaen J., De Berardinis V., Raoult C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volkoff J.N., Guigo R., Zody M.C., Mesirow J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn M., Robinson-Rechavi M., Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C., Wincker P., Landre B.S., Weissenbach J., Roest Crollius H., RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; RT Nature 431:946-957 (2004). RN [2]
Q4LE81_HUMAN PRELIMINARY;	AC	NUCLEOTIDE SEQUENCE.
Q4LE81_HUMAN PRELIMINARY;	CC	Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
AC Q4LE81	CC	- - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DT 13-SEP-2005 (TREMBLrel. 31, Created)	DR	EMBL; CAAE01015003; CG090987.1; -; Genomic_DNA.
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	FT	NON_TER 1 1
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)	FT	NON_TER 456 456
DE PDE7B variant protein (Fragment).	SQ	SEQUENCE 456 AA; 52118 MW; 60B4805381D70669 CRC64;
OS Homo sapiens (Human);	Qy	Query Match Score 1280; DB 2; Length 586;
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrates; Primates; Catarrhini; Hominoidea;	Qy	Best Local Similarity 100.0%; Pred. No. 4.2e-100;
OC NCBI_TaxID=9606;	Qy	Mismatches 0; Indels 0;
QX RN NUCLEOTIDE SEQUENCE.	RC	7 ERGEGLFLENPDONAKCVCML-----GDIRL_RQGTG_YRAERGSGYP 47
QX TISSUE=Brain; Saito K., Yamakawa H., Kikuno R.F., Nakayama M., Nakajima D., Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.; RT "Preparation of a set of expression-ready clones of mammalian long cDNAs encoding large proteins by the ORF trap cloning method."; RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. DR EMBL; AB209990; BAB06072.1; -; mRNA.	Db	1 QRGAVNLTSPEQNAQVRMLDHRVDRNPKHLPAASTAECKLSTGHAGYLVERGSGYP 60
QX SEQUENCE 586 AA; 66230 MW; F964F0549A9F88D CRC64;	Qy	84 FIDFRLLNNTSYSGEGTKKVKRLLSFQYFHASBLLRG 87
FT NON_TER 1 1	Db	61 LIDQVLKSSSQGEVAQTRRVRQLQSFRQTCASRLLRGFLVAPLSLHLDDGYLG 120
QX SEQUENCE 586 AA; 66230 MW; F964F0549A9F88D CRC64;	Qy	88 IIPQAPLHLDDELYGQARHMLSKYGMWDFDIFLFLFDRLTNNSLYLTLCLHFNTGLIHH 147

Db	121	QAAHMLSKVGTWNFDI_FLFDRLTNGSLVLMCHLENVYGLVHFEQLDNVKLHRFLGMVQ	180	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Qy	164	EDYHSQNPNVNAHADTVQAMHCYKLKEPKLASFTPLDILMGLAAAHHDVDPGYNCP	223	OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Db	181	EDYHSQNPNVNAHADTVQAMHCYKLKEPKLAESPLDVFLGLMAAAAHHDVDPGYNQP	240	OC	Muridae; Murinae; Mus.
Qy	224	FLIKTNWHHLANLY----QNSVLESHWSTGMRSSRLLAHLPKEMT	268	NCBI_TaxID=1090;	
Db	241	FLIKTRHHHLASLYQVHQSVQNTSVLESHTWSTGMLRESGGLSHLPADM	291	RN	
RESULT 9					
Q8VIE3_	RAT	PRELIMINARY;	PRT;	359 AA.	
ID	QBVIE3_	RAT			
AC	Q8VIE3_	RAT			
DT	01-MAR-2002	(TREMBrel. 20, Created)			
DT	01-MAR-2002	(TREMBrel. 20, Last sequence update)			
DT	01-MAR-2004	(TREMBrel. 26, Last annotation update)			
DE	Cyclic nucleotide phosphodiesterase 7B3	(EC 3.1.4.17).			
GN	Name=Pde7B; Synonyms=rNDE7B;				
OS	Rattus norvegicus (Rat).				
OC	Mammalia; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC	Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Rattus;				
OX	NCBI_TaxID=10116;				
RN					
NUCLEOTIDE SEQUENCE.					
RA	TISSUE=Testis;				
RA	Sasaki T.; Kotera J.; Omori K.;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB057410; BAB79638.1;	- ; mRNA.			
DR	HSSP; Q8B499; IOYN.				
DR	RGD; 623016; Pde7B.				
DR	GO; GO:004144; P13' ,5'-cyclic-nucleotide phosphodiesterase activity; IEA.				
DR	GO; GO:0016787; Hydrolase activity; IEA.				
DR	GO; GO:0007165; Signal transduction; IEA.				
DR	InterPro; IPR03607; Met_phos_hydro.				
DR	InterPro; IPR02073; PDBase.				
DR	Pfam; PF00233; PDbase_I; 1.				
DR	PRINTS; PRO0387; PDIBESTERASE1.				
DR	SMART; SM00471; HPC; 1.				
DR	PROSITE; PS00126; PDEASE_I; UNKNOWN_1.				
KW	Hydrolyase.				
SQ	SEQUENCE: 359 AA; 41456 MW; QEF7272737GB48A CRC64;				
Qy	Query Match Score 953; DB 2; Length 359;				
Best Local Similarity 98.3%; Pred. No. 1..86-78;					
Matches 176; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
Qy	90 PQAPLHLLDGDYLGQARHMLSKVGMWDIFLFDRLTNGSLVLLCHFNTGLHHFK 149				
Db	3 PQAPLHLLDGDYLGQARHMLSKVGMWDIFLFDRLTNGSLVLLCHFNTGLHHFK 62				
Qy	150 LDWYTLHRLPVMQDYDHSONPYHNAHADTVQAMHCYKLKEPKLASFTPLDIMGILA 209				
Db	63 LDWYTLHRLPVMQDYDHNPYHNAHADTVQAMHCYKLKEPKLASFTPLDIMGILA 122				
Qy	210 AAAHDVDHGVNQPLKTHNLANLYQMSVLENHHRSTGMLRESRLLAHLPKEMT 268				
Db	123 AAAHDVDHGVNQPLKTHNLANLYQMSVLENHHRSTGMLRESRLLAHLPKEMT 181				
RESULT 10					
Q655G2_MOUSE	PRELIMINARY;		PRT;	482 AA.	
ID	Q655G2_MOUSE				
AC	Q655G2;				
DT	05-JUL-2004 (TREMBrel. 27, Created)				
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)				
DE	Pde7a protein.				
GN	Name=Pde7a;				
OS	Mus musculus (Mouse).				
Qy	247 WRSTIGMLRESRLLAHLPK 266				
Qy	286 WRSAGVLLIRESGLFSHPLPE 305				
Db	RESULT 11				
PDB7A_MOUSE	STANDARD;				
ID	PDB7A_MOUSE				
AC	P70453; Q9ERB3;				
PRT;	456 AA.				

DT	15-JUL-1998 (Rel. 36, Last sequence update)	SQ	SEQUENCE	456 AA;	52442 MW;	0B826B96490D9F6B CRC64;
DT	10-MAY-2005 (Rel. 47, Last annotation update)	Query Match	59.3%;	Score 913;	DB 1;	Length 456;
DE	High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A (EC 3.1.4.17) (P2A);	Best Local Similarity	65.8%;	Pred. No. 1.e-74;		
DE	(EC 3.1.4.17) (P2A);	Matches	53;	Mismatches	53;	Gaps 0;
GN	Name=Pde7a;					
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii; Muroidea; Muridae; Murinae; Mus.	Qy	7 ERGCEBILFPNDQNAKCVMLGDIRLRLCQTGVDAERRSSYFIDFLRLNSTTYSGEIGTK 66			
OC		Db	20 KRRGAISYDSSDQTALYIIRMLGDVRVSRAFGFETRGSHPYIDRIFHSQSIEAVSA 79			
OC		Qy	67 KKYKRLLSFORYPHASRLURGIIPOAQLHLDDEDYLGQARHMLSKVGWMDFDIFLFDRLT 126			
OC		Db	80 RNIRRLLSFORYLRSRVSFRATVCSLDLDEYNGQAKCMLEKGWNFDFIFLFDRLT 139			
OX		Qy	127 NGNSLVTLICHLFNTGLJHHFKLDMYLTHRELWYDHYSONPYRNVAHAADVTQAMH 186			
RN		Db	140 NGNSLVLSTLTHFLSLHGLEYFHDLMLKLRFVLMIQDHYSONPYRNVAHAADVTQAMH 199			
RC	NUCLEOTIDE SEQUENCE (ISOFORM 1).	Qy	187 CYLKPKLASSFLPLDIMGLLAAAHDVDPGYNQPPLIKTMHNLANYQMSVLENH 246			
TC	TISSUE=Skeletal muscle; MEDLINE=97098542; PubMed=8943082; DOI=10.1073/prnas.93.24.14188;	Db	200 CYLKPKLASSVTPWDILSLSLAAATHLDPGYNQPPLIKTMHNLATYKNSSVLENH 259			
RA	Beavo J.J., Beavo J.A.; "Identification and tissue-specific expression of PDE7 phosphodiesterase splice variants"; Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).	Qy	247 WRETTIGMRLRESRLLAHLPK 266			
RT		Db	249 WRSAGVGLRESGLFSHPLE 279			
RN		Db	260 WRSAGVGLRESGLFSHPLE 279			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).					
RC	TISSUE=brain, and Testis; MEDLINE=20483661; PubMed=11027622; DOI=10.1006/bbrc.2000.3613;	RESULT 12				
RA	Wang P., Wu P., Egan R.W., Billah M.M.; "Cloning, characterization, and tissue distribution of mouse phosphodiesterase 7A1"; Biochem Biophys. Res. Commun. 276:1271-1277(2000).	Q96772 HUMAN PRELIMINARY;				
RT		ID Q96772_HUMAN PRELIMINARY;				
RT		AC Q96772;				
RT		DT 01-DEC-2001 (TREMBLrel. 19, Created)				
RT		DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
RT		DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
RT		DE CAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.				
RT		OS Homo sapiens (Human)				
RT		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo				
RL		OC NCBI_TAXID=9606;				
CC	-!- FUNCTION: Plays a role in signal transduction by regulating the intracellular concentration of cyclic nucleotides. This phosphodiesterase is highly specific for cAMP and may have a role in muscle signal transduction.	OX [1]				
CC	-!- CCATYTIC ACTIVITY: Adenosine 3', 5'-cyclic phosphate + H(2)O = adenosine 5'-phosphate.	RN NUCLEOTIDE SEQUENCE.				
CC	-!- COFACTOR: Divalent cations.	RX MEDLINE=21265467; PubMed=11371644; DOI=10.1073/pnas.101131098;				
CC	-!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.	RA Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.; RT "T cell activation up-regulates cyclic nucleotide phosphodiesterases				
CC	-!- PATHWAY: Cyclic nucleotide metabolism.	RL PROC. NATL. ACAD. SCI. U.S.A. 98:6319-6324 (2001).				
CC	-!- ALTERNATIVE PRODUCTS:	DR EMBL: AP332652; AAK57640.1; -; mRNA.				
CC	-!- Comment=Additional isoforms seem to exist;	DR GO; GO:0004114; F:3;, 5'-cyclic-nucleotide phosphodiesterase a. . . IEA.				
CC	Name1=Synonyms=pub7A2;	DR GO; GO:0016787; F:hydrolyase activity; IEA.				
CC	Name2=Synonyms=Display;	DR GO; GO:0007165; P:signal transduction; IEA.				
CC	Isoid=P70455-1; Sequence=Displayed;	DR InterPro; IPR036307; Net_phos_hydro.				
CC	Isoid=pub7A1;	DR Pfam; PF00233; PDBase I; 1.				
CC	Isoid=P70455-2; Sequence=VSP_00594;	DR PRINTS; PR00387; PDBase I.				
CC	-!- TISSUE SPBCIFICITY: Widely expressed with highest levels in the skeletal muscle.	DR SMART; SMO0471; HDC; I.				
CC	-!- DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.	DR PROSITE; PS00126; PDEASE I; UNKNOWN 1.				
CC	-!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.	DR SEQUENCE; PS00126; PDEASE I; UNKNOWN 1.				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	SQ Query Match	58.9%;	Score 907;	DB 2;	Length 424;
CC		Best Local Similarity	64.6%;	Pred. No. 3.5e-74;		
CC		Matches	168;	Mismatches	53;	Gaps 0;
CC		PROSITE; PS00126; PDEASE I.				
CC		DR 46 QRGRCAISYDSSDQTALYIIRMLGDVRVSRAFGFETRGSHPYIDRIFHSQSIEAVSA 105				
CC		Qy 67 KKYKRLLSFORYPHASRLURGIIPOAQLHLDDEDYLGQARHMLSKVGWMDFDIFLFDRLT 126				
CC		Db 106 RNIRRLLSFORYLRSRVSFRATVCSLDLDEYNGQAKCMLEKGWNFDFIFLFDRLT 165				
FT	VARSPLIC 1 20 MGITIWCAALVLIKWTSK -> MEVCYQLPVNPLDRPVP QHVISRGATFSSSALGPCHPRLQSC (in isoform 2).	FT /FTid=VSP_004594.				
FT	CONFlict 407 407 A -> D (In Ref. 2).					

QY		127	NGNSLYTLLCLHLNTHGLIHFPLKDMVTLERFLWVQEDHPSQYHNAHAADTVQAMH	186
Db		166	NGNSLYTLLPHLSPHLSLHGLIEYMMKLRFLMVKQEDHPSQYHNAHAADTVQAMH	225
QY		187	CYKEPKLAKASFLPLDMLGLLAAAHDDVHPGVNQPFLIKTNHHLANLYQNMSVLENH	246
Db		226	CYKEPKLANSVTPDLSLIAAATHDLPGVNQPFLIKTNHLYLATIYKNTSVLENH	285
QY		247	WRSTIGMLRESRLLAHLPLKE	266
Db		286	WRSAYVLLRSGLEFSHLPLKE	305
RESULT 13				
PDE7A_HUMAN		STANDARD;	PRT;	482 AA.
ID	Q13946;	O13380;		
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	10-MAY-2005	(Rel. 47, Last annotation update)		
DE	High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A (EC 3.1.4.17) (HCP1) (TM22).			
Name=	PDE7A;			
GN	Homo_sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
Mammalia;	Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
HO	Homeo_ TaxID=9606;			
OX				
RN	NUCLEOTIDE SEQUENCE (ISOFORM PDE7A1).			
MEDLINE#93286141; PubMed=8339765;				
Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,				
Riggs M., Rodgers J., Beavo J.A., Wiger M.;				
"Isolation and characterization of a previously undetected human cAMP				
phosphodiesterase by complementation of cAMP phosphodiesterase-				
deficient Saccharomyces cerevisiae."				
J. Biol. Chem. 266:12925-12932 (1993)."				
[2]	NUCLEOTIDE SEQUENCE (ISOFORM PDE7A2).			
TISSUE=skeletal muscle;				
MEDLINE#97341143;				
RT	Han P., Zhu X., Michaeli T.,			
RT	"Alternative splicing of the high affinity cAMP-specific			
RT	phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";			
J. Biol. Chem. 272:16152-16157 (1997).				
-i-	FUNCTION: Plays a role in signal transduction by regulating the			
intracellular concentration of cyclic nucleotides. This				
phosphodiesterase is highly specific for cAMP and may have a role				
in muscle signal transduction.				
-i-	CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =			
adenosine 5'-phosphate.				
-i-	COFACTOR: Divalent cations.			
-i-	PATHWAY: Cyclic nucleotide metabolism.			
-i-	SUBCELLULAR LOCATION: PDE7A1 (57 kDa) is located mostly to soluble			
cellular fractions. PDE7A2 (50 kDa) is located to particulate				
-i-	ALTERNATIVE PRODUCTS:			
Event=Alternative splicing; Named isoforms=2;				
Name=PDE7A1;				
IsoID=Q13946-1; Sequence=Displayed;				
Name=PDE7A2;				
IsoID=Q13946-2; Sequence=VSP 004593;				
-i-	TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal			
muscle and at low levels in a variety of tissues including brain				
and heart. It is expressed as well in two T-cell lines. PDE7A2 is				
found abundantly in skeletal muscle and at low levels in heart.				
-i-	DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2			
are found in several fetal tissues, expression is reduced				
throughout development. It persists strongly only in adult				
skeletal muscle.				
-i-	DONIN: Composed of a C-terminal catalytic domain containing two			
putative divalent metal sites and an N-terminal regulatory domain.				
NCBI_TaxID=9600;				
RN	NUCLEOTIDE SEQUENCE;			
TISSUE=Kidney;				
RC	RC			

The German cDNA Consortium;
 RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 Submitted (NOV 2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CRB60948; CAB93051; -; mRNA.
 GO; GO:004114; F3',5'-cyclic-nucleotide phosphodiesterase activity; IEA.
 GO; GO:0016787; Hydrolase activity; IEA.
 GO; GO:0007165; Signal transduction; IEA.
 DR InterPro; IPR003607; Met phos_hydro.
 DR InterPro; IPR002033; PDEase.
 DR Pfam; PF00233; PDEase_1.
 DR PRINTS; PR00387; PDEESTERASE1.
 SMART; SM00471; HIC; 1.
 PROSITE; PS00126; PDEASE_1; UNKNOWN_1.
 DR HYPOTHETICAL protein.
 KW SEQUENCE 456 AA; 5275 MW; CB162B0BREF074BF CRC64;

SEQUENCE :
 58.8% Score 906; DB 2; Length 456;
 Best Local Similarity 64.6%; Pred. No. 4.7e-74;
 Matches 16; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
 DR QY 7 ERCGEFLFEPNDQDAKCVCMGLDRLRGTCVRAERRGGPFIDFRLLNNTTYSGEIICK 66
 DR 20 KRRGAGSVSSDQDALYTMGLDVRSRSGAFESERRGGSHPYIDFRIFQSLEEVSYSA 79
 DR QY 67 KVKRLLSFORYFHASRLRGLITIQAPLHLDEYLQRHRHMSKVGMWDFDIFLFDLT 126
 DR 80 RNRVLLSFORYLSSRSPRFTAVNSNLILDDYNGQKRCMLERGVWNEDFLFDLT 139
 DR QY 127 NGNSLVUTLCHLFNTFHGLTHFKLDMVTLHREFLYVQDSDYHSQNPYNAVAADVTQAMH 186
 DR 140 NGNSLVSLTHLFSLHGLLYFHFLDMCARRFLKQYDHSQNPYNAVAADVTQAMH 199
 DR QY 187 CYLKPKKLASFLTDIMGLLAAAHDDTHPGUNPQLIKTNHLYQMSVLENHH 246
 DR 200 CYLKPKKLANSVTDWLSSLIAATHDDHPGYNQPLIKTNHLYLATLYQMSVLENHH 259
 DR QY 247 WRSTIGMLBESRLLAHLPE 266
 DR 260 WRSAGVGLLSESGLFSHLPE 279
 DR RESULT 15
 ID PDE7A RAT STANDARD; PRT; 426 AA.
 AC 008593;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE High-affinity cAMP-specific phosphodiesterase 7A
 DE (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
 DE (Fragment)
 GN Name=Pde7a;
 OS Rattus norvegicus (Rat);
 TISSUE=Brain;
 RX MEDLINE=98176136; PubMed=9515162;
 RA Hoffmann R., Abdei'Al S., Engels P.;
 RT "different distribution of rat PDE-7 mRNA in embryonic and adult
 rat brain.";
 RL Biochem. Biophys. 28:103-113 (1998).
 CC -!- FUNCION: Plays a role in signal transduction by regulating the
 intracellular concentration of cyclic nucleotides. This
 phosphodiesterase is highly specific for cAMP and may have a role
 in muscle signal transduction (By similarity).
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 adenosine 5'-phosphate
 CC -!- COFACTOR: Divalent cations (By similarity).

CC -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By similarity).
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; U77880; AAB51234.1; -; mRNA.
 DR HSSP; Q08499; 1MFD.
 DR RCD; 68391; Pde7a.
 DR InterPro; IPR003607; Met_phos_hydro.
 DR InterPro; IPR02073; PDEase.
 DR Pfam; PF00233; Pdase_1; 1.
 DR PRINTS; PR00387; PDESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_1; 1.
 DR CAMP; Hydrolase.
 FT REGION 131 395 Catalytic (By similarity).
 SQ SEQUENCE 426 AA; 49274 MW; 129BD01C9315D26 CRC64;
 DR Query Match 57.9%; Score 892; DB 1; Length 426;
 DR Best Local Similarity 66.7%; Pred. No. 8.3e-73;
 DR Matches 166; Conservative 33; Mismatches 50; Indels 0; Gaps 0;
 DR FT REGION NON_TER 1 1
 DR SQ .Y 18 DONAKCVCMLGDIRLRGQTQVRAERGSYPPIDFRFLNSTTYSGEIGTKKKVKRLLSFOR 77
 DR 1 DQDTALYTRNLGDYVRSSAGFETGRGSHPYIDFRIFHAQSEEAWSVARNTRRLSFOR 60
 DR .Y 78 YFHASRLLRGLITQAPLHLDEDYLQRHRHMSKVGMWDFDIFLFDLTNGNSLYVLLCH 137
 DR 61 YLRSSRERFRGATVCRSLNLTDEYNGQAKCMLEKVGNNNFIDFLFDLTNGNSVSLTFH 120
 DR .Y 138 LFPNTGLLTHFKLDMVTLHREFLYVQDSDYHSQNPYNAVAADVTQAMHCLKEPKLANS 197
 DR 121 LFSLHGLLEYFHLMVKLRRFLWIQDYSQNPYNAVAADVTQAMHCLKEPKLANS 180
 DR .Y 198 LTPLDIMIGLLLAAAHDYDHPGYNQPLIKTNHHLANLYQMSVLENHWRSPTGMLRES 257
 DR 181 VTPWDILLSLIANATHDLPQGYNQPLIKTNHLYLATLYQMSVLENHWRSAVLILRES 240
 DR .Y 258 RLLAHLPKE 266
 DR 241 GLPSHLPLE 249
 DR
 DR Search completed: March 10, 2006, 20:02:06
 Job time : 124.155 secs

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GenCore version 5.1.7						
Copyright (c) 1993 - 2006 Biocceleration Ltd.						
A protein - protein search, using sw model						
Run on: March 10, 2006, 20:02:25 ; Search time 26.1463 Seconds (without alignments)						
Number of hits satisfying chosen parameters: 572060						
Minimum DB seq length: 0 Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0% Listing first 45 summaries						
Database : Issued Patents AA.*						
1: /cggn2_6/ptodata/1/iaa5_-COMB_.pep:*						
2: /cggn2_6/ptodata/1/iaa6_-COMB_.pep:*						
3: /cggn2_6/ptodata/1/iaaH_-COMB_.pep:*						
4: /cggn2_6/ptodata/1/iaaPCTUS_COMB_.pep:*						
5: /cggn2_6/ptodata/1/iaaRE_COMB_.pep:*						
6: /cggn2_6/ptodata/1/iae/backfile1.pep:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
* Query Match Score Length DB ID Description						
1	1280	83.1	320	2	US-09-330-970-3	Sequence 3, Appli
2	1280	83.1	502	2	US-09-330-970-1	Sequence 1, Appli
3	1073	69.7	390	2	US-09-949-016-10020	Sequence 10020, A
4	907	58.9	498	1	US-07-388-319C-20	Sequence 20, Appli
5	907	58.9	498	1	US-09-474-319C-20	Sequence 20, Appli
6	907	58.9	498	2	US-09-146-249A-20	Sequence 20, Appli
7	907	58.9	498	2	US-08-206-188B-20	Sequence 20, Appli
8	331.5	21.5	517	2	US-09-602-735B-4	Sequence 4, Appli
9	330.5	21.5	451	1	US-08-174-319C-61	Sequence 61, Appli
10	330.5	21.5	451	2	US-09-146-249A-61	Sequence 61, Appli
11	330.5	21.5	451	2	US-08-206-188B-61	Sequence 61, Appli
12	330.5	21.5	518	2	US-09-602-735B-2	Sequence 2, Appli
13	330.5	21.5	673	1	US-08-577-492-35	Sequence 35, Appli
14	330.5	21.5	673	1	US-08-474-319C-63	Sequence 63, Appli
15	330.5	21.5	673	2	US-09-146-249A-63	Sequence 63, Appli
16	330.5	21.5	673	2	US-08-206-188B-63	Sequence 63, Appli
17	330.5	21.5	673	1	US-09-019-630-35	Sequence 35, Appli
18	323	21.0	302	4	PCT-US91-02714-21	Sequence 21, Appli
19	323	21.0	398	1	US-08-474-319C-95	Sequence 86, Appli
20	323	21.0	638	1	US-07-688-521B-8	Sequence 22, Appli
21	323	21.0	734	2	US-09-146-249A-85	Sequence 85, Appli
22	323	21.0	734	2	US-08-206-188B-85	Sequence 85, Appli
23	320.5	20.8	686	1	US-08-942-521B-8	Sequence 9, Appli
24	320.5	20.8	885	1	US-08-577-492-33	Sequence 33, Appli
25	320.5	20.8	885	2	US-09-079-630-33	Sequence 33, Appli
26	320.5	20.8	886	1	US-09-146-249A-65	Sequence 65, Appli
27	320.5	20.8	886	1	US-09-174-319C-65	Sequence 65, Appli

Sequence 1, Application US/09330970
 Patent No. 6146816
 GENERAL INFORMATION:
 APPLICANT: Robison, Keith E.
 APPLICANT: Kapeiler-Libermann, Rosana
 APPLICANT: White, David
 TITLE OF INVENTION: A No. 6146876 Human Cyclic Nucleotide
 TITLE OF INVENTION: Phosphodiesterase
 FILE REFERENCE: 5800-28
 CURRENT APPLICATION NUMBER: US/09/330,970
 FILING DATE: 1999-06-11
 EARLIER APPLICATION NUMBER: 09/277,423
 EARLIER FILING DATE: 1999-03-26
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-330-970-1

RESULT 4
 US-07-688-352C-20
 Query Match 83.1%; Score 1280; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 7.4e-140;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 28 GDILRGQTGVRARRGSPPIDRLNNTTYSGEIGYKKVRLLSQFRYFHASRLRIG 87
 Db 80 GDILRGQTGVRARRGSPPIDRLNNTTYSGEIGYKKVRLLSQFRYFHASRLRIG 87
 Qy 88 IIPQAPLHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTGLIHH 147
 Db 140 IIPQAPLHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTGLIHH 199
 Qy 148 FKLDMVTLHFLM/QEDTHSQQPYHNAADVTOAMCYKLEPKLASFLPLDIMG 207
 Db 200 FKLDMVTLHFLM/QEDTHSQQPYHNAADVTOAMCYKLEPKLASFLPLDIMG 259
 Qy 208 LAAAHHDVHPGTNQPLIKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 267
 Db 260 LAAAHHDVHPGTNQPLIKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 319
 Qy 268 T 268
 Db 320 T 320

RESULT 3
 US-09-949-016-10020
 Sequence 10020, Application US/09949016
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO 10020
 LENGTH: 390
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-10020
 Query Match 69.7%; Score 1073; DB 2; Length 390;
 Best Local Similarity 86.7%; Pred. No. 6.1e-116;

Matches 208; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 29 DIRLRGQTGVRARRGSPPIDRLNNTTYSGEIGYKKVRLLSQFRYFHASRLRIG 88
 Db 1 DIRLRGQTGVRARRGSPPIDRLNNTTYSGEIGYKKVRLLSQFRYFHASRLRIG 60
 Qy 89 IIPQAPLHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTGLIHF 148
 Db 61 IIPQAPLHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTGLIHF 99
 Qy 149 KLDMVTLHFLM/QEDTHSQQPYHNAADVTOAMCYKLEPKLASFLPLDIMG 208
 Db 100 -----
 Qy 209 AAAAHHDVHPGTNQPLIKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEMT 268
 Db 149 AAAAHHDVHPGTNQPLIKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEMT 208

RESULT 4
 US-07-688-352C-20
 Sequence 20, Application US/07688352C
 Patent No. 5527896
 GENERAL INFORMATION:
 APPLICANT: Wigler, Michael H.
 APPLICANT: Colicelli, John J.
 TITLE OF INVENTION: Cloning by Complementation and Related
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Bicknell
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/688,352C
 FILING DATE: 19910419
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25447
 REFERENCE DOCKET NUMBER: 27805/30197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5150
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-07-688-352C-20

Query Match 58.9%; Score 907; DB 1; Length 498;
 Best Local Similarity 64.6%; Pred. No. 1.8e-96;
 Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
 Qy 7 ERGEELIFENPDQNACKVCMGLDIRLRGQTGVRARRGSPPIDRLNNTYSGEIGTK 66
 Db 62 QRGRGALSYDSSDQTALEYMLGDVRRSRAFESERGSHPYTDERRFHQSQEIEVSVA 121

RESULT 5
US-10-474-379C-20
Sequence 20 : Application US/08474379C
Patent No. 5977305

GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.

TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED PROCESSES

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 498 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein

RESULT 6
US-09-146-249A-20
Sequence 20 : Application US/09146249A
Patent No. 6063940

GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related Processes

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 498 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 58.9%; Score 907; DB 1; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Query 7 ERCGRLFFENPDQNAKCVMLGDIRLGGTGVRAERRGGYPFDRLINNSTYSGEIGK 66
Db 62 QRREGAISDSSDQTALYIIRMLGDYVRSAAGPESERRGSHPYIDFRIFHSQSEIEVSVA 121

Qy 67 KKVKRLLSFQRYFHASRLLRGIIPOAQLLILDEDYLQARHMLSKVGMWDFDIFLPDRLT 126
 Db 122 RNTIRLLSPLRSRGRGTAWSNLSNLDDYNGQAKCMLEKVGWNNFDFLPDRLT 181

Qy 127 NGNSLVTLLCHLFNTGLJHHFKLDMVTLHREFLVMQEDYHSNQPYHNAVAADTVQAMH 186
 Db 182 NGNSLVSLSPLFHLSLGLJEYFLDMKMLKRRFLVMQEDYHSNQPYHNAVAADTVQAMH 241

Qy 127 NGNSLVTLLCHLFNTGLJHHFKLDMVTLHREFLVMQEDYHSNQPYHNAVAADTVQAMH 186
 Db 182 NGNSLVSLSPLFHLSLGLJEYFLDMKMLKRRFLVMQEDYHSNQPYHNAVAADTVQAMH 241

Qy 187 CYLKPKLASFELTPLDILMGLLAAAHDYDHPGVNQPELIKTNNHHLANLYONMSVLENHH 246
 Db 242 CYLKPKLANSVTPWDILSLIAATHDLDHPGVNQPELIKTNNHHLATLYKOTSVLENHH 301

Qy 187 CYLKPKLASFELTPLDILMGLLAAAHDYDHPGVNQPELIKTNNHHLANLYONMSVLENHH 246
 Db 242 CYLKPKLANSVTPWDILSLIAATHDLDHPGVNQPELIKTNNHHLATLYKOTSVLENHH 301

Qy 247 WRSTIGMRESRLLAHLPE 266
 Db 302 WRSAVGLLRESGFSLHPLPE 321

Qy 247 WRSTIGMRESRLLAHLPE 266
 Db 302 WRSAVGLLRESGFSLHPLPE 321

RESULT 8
 US-09-602-735B-4
 ; Sequence 4, Application US/09602735B
 ; Patent No. 6656717
 ; GENERAL INFORMATION:
 ; APPLICANT: Xir, Xiaonan
 ; ADDRESS: Unterbeck, Axel
 ; INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
 ; Use
 ; TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
 ; Use
 ; FILE REFERENCE: 453260-55
 ; CURRENT APPLICATION NUMBER: US/09/602,735B
 ; CURRENT FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: U.S. 60/141,196
 ; PRIOR FILING DATE: 1999-06-25
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-602-735B-4

Query Match 21.5%; Score 331.5; DB 2; Length 517;
 Best Local Similarity 37.8%; Pred. No. 1.7e-29; Indels 9; Gaps 4;

Matches 74; Conservative 35; Mismatches 78; Del 66 KKVKVRLLS---FORYFHASRLLRGIIPOAQLLILDEDYLQARHMLSKVGMWDFDIFL 121
 Db 63 KEKKRPMQSISGVKLMHSSSLTNSCIPRFGVKTQBDVLAKE--LEDVNKWGHLVFR 119

Db 122 FURLTNGNSLVTLLCH-LFNTGLHFLKDMVTLHREFLVMQEDYHSNQPYHNAVAAD 180
 Qy 120 IAEL-SGNRPLRPTMFTQERDLKTFKIPDFTLMLTLEDHTHADYHNNHAAAD 178

Qy 181 VTOQAMHCVLKEPKLASFELTPLDILMGLLAAAHDYDHPGVNQPELIKTNNHHLANLYONMS 240
 Db 179 VVQSTHVLSTPALEAVFTDLEIALLAFASATHDVBHPGVSNQFLINTSELAMMNDSS 238

Qy 241 VLENHHRSTICMRE 256
 Db 239 VLENHHLAVGFKLQE 254

RESULT 9
 US-08-474-379C-61
 ; Sequence 61, Application US/08474379C
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; ADDRESS: 1000 University City Science Center, Philadelphia, PA 19104
 ; PATENT NO.: 597305
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6100 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois

Qy 7 ERGEIILPENPDONAKCVCMLGDIPRLRSQTCGYRAERGSYPIDFRLUNSTRSYSGEITK 66
 Db 62 QRGAISDSDOTDIALYIPLMGDVYRSEFSEGRSHPYDFRIFPSQSBIEEVSA 121

Qy 67 KKVKRLLSFQRYFHASRLLRGIIPOAQLLILDEDYLQARHMLSKVGMWDFDIFLDRLT 126
 Db 122 RNTIRLLSPLRSRGRGTAWSNLSNLDDYNGQAKCMLEKVGWNNFDFLPDRLT 181

COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/146,249A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/206,188
 FILING DATE: 01-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/688,352
 FILING DATE: 19-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 27866/32771
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-474-379c-61

Query Match 21.5%; Score 330.5; DB 2; Length 451;
 Best Local Similarity 37.8%; Pred. No. 1.8e-29;
 Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVRLLS ---FORYFHASRLRGIIPOAPLHLDDEDYLGQARHMSKVGMDFDIPL 121
 Db 234 KEKKRPMQSISGVKLRAHSSLTSSPFGVTEQDVLAKE--LEDVNKGHLVER 290

Query Match 21.5%; Score 330.5; DB 2; Length 451;
 Best Local Similarity 37.8%; Pred. No. 1.8e-29;
 Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 122 FDRLTNGNSLVTLICH-LFNTNGLHFKLDMVTLHRELYMVOEDYHSQNPYHNAVAHD 180
 Db 291 IAEI-SGNRPLTVHTRIFOBRLKTFCPVDTLITYMLTEPHYHADVAHNNAHD 349

Qy 181 VTOQAMHCYLKEPKLASFLTDIMGLLLAAAHDVDPGSYNQPLIKTNHHLANYQNM 240
 Db 350 VVQSTHVLLSTPALEAVFTDLEILAAIFSAIHVDHPGSVSNQPLINTNSEALMYNDSS 409

Qy 241 VLENHHRSTIGMR 256
 Db 410 VLENHHLAVGFQLLQR 425

RESULT 11
 US-08-206-188B-61
 Sequence 61, Application US/08206188B
 ; Sequence 61, Application US/08206188B
 ; Patent No. 6100025
 ; GENERAL INFORMATION:
 ; ADDRESSEE: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; PROCESSES
 ; NUMBER OF SEQUENCES: 84
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.10
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/206,188B
 ; FILING DATE: 01-MAR-1994

RESULT 10
 US-09-146-249A-61
 Sequence 61, Application US/09146249A
 ; Sequence 61, Application US/09146249A
 ; Patent No. 6069240
 ; GENERAL INFORMATION:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 ATTORNEY / AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-206-188B-61

Query Match Score 330.5; DB 2; Length 451;
 Best Local Similarity 37.8%; Pred. No. 1.8e-29; Indels 9; Gaps 4;
 Matches 74; Conservative 35; Mismatches 78;

Qy 66 KCKVKRLLS---FORYFHASRLRLRGITIPOAQLHLDDEYLGOARHMLSKVGMWDFDIFL 121
 Db 234 KEKCKRPMSQISGVKKMHSSTNSSSLTNPQFLINTNSSELALMYNDS 256

Qy 122 FDRLTNGNSLVTLLCH-LFNTHGLJHHFKLDMYTLHRFLVYQEDYHSQNPYHNAHAD 180
 Db 291 IAEI-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITYLMTLEDHYHADAVHNINHAD 349

Qy 181 VTQAMHCYKEPKLASFLPFLDIMGLLAAAADHDVHPVNVQPLIKTNHHLANLYQMS 240
 Db 350 VVQSTHVLLSTPALEAVFTDLEILAAIFFSAIHVDHPVCSNQFLINTNSSELALMYNDS 409

Qy 241 VLENHHWRSTIGLRE 256
 Db 410 VLENHHLAVGFKLQE 425

RESULT 12
 US-09-602-735B-2
 Sequence 2, Application US/09602735B
 Patent No. 6656717
 GENERAL INFORMATION:
 APPLICANT: Xin, Xiaonan
 APPLICANT: Unterbeck, Axel
 APPLICANT: Hu, Yinghe
 TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of Use
 FILE REFERENCE: 453460-55
 CURRENT FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: U.S. 60/141,196
 PRIOR FILING DATE: 1999-06-25
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 2
 LENGTH: 518
 TYPE: PRO
 ORGANISM: Homo sapiens
 US-09-602-735B-2

Query Match Score 330.5; DB 2; Length 518;
 Best Local Similarity 37.8%; Pred. No. 2.2e-29; Indels 9; Gaps 4;
 Matches 74; Conservative 35; Mismatches 78;

Qy 66 KCKVKRLLS---FORYFHASRLRLRGITIPOAQLHLDDEYLGOARHMLSKVGMWDFDIFL 121
 Db 63 KEKCKRPMSQISGVKKMHSSTNSSSLTNPQFLINTNSSELALMYNDS 211
 Qy 122 FDRLTNGNSLVTLLCH-LFNTHGLJHHFKLDMYTLHRFLVYQEDYHSQNPYHNAHAD 119

Db 120 IAEI-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITYLMTLEDHYHADAVHNINHAD 178
 181 VTQAMHCYKEPKLASFLPFLDIMGLLAAAADHDVHPVNVQPLIKTNHHLANLYQMS 240
 179 VVQSTHVLLSTPALEAVFTDLEILAAIFFSAIHVDHPVCSNQFLINTNSSELALMYNDS 238

Qy 241 VLENHHWRSTIGLRE 256
 Db 239 VLENHHLAVGFKLQE 254

RESULT 13
 US-08-577-492-35
 Sequence 35, Application US/08577492
 Patent No. 5851784
 GENERAL INFORMATION:
 APPLICANT: Owens, Raymond John
 APPLICANT: Perry, Martin John
 APPLICANT: Lumb, Simon Mark
 TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 5851784r1s
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/577,492
 FILING DATE: 22-DEC-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9426227.6
 FILING DATE: 23-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9512996.1
 FILING DATE: 26-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Cherry, David A.
 REGISTRATION NUMBER: 35,099
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 US-08-577-492-35

Query Match Score 330.5; DB 1; Length 673;
 Best Local Similarity 37.8%; Pred. No. 3.3e-29; Indels 9; Gaps 4;
 Matches 74; Conservative 35; Mismatches 78;

Qy 66 KKVKVRLS---FQRYPHASRLRGITIPOAQLHLDDEYLGOARHMLSKVGMWDFDIFL 121
 Db 218 KERKKRPMQSISGVKKMHSSTNSSSLTNPQFLINTNSSELALMYNDS 274
 122 FDRLTNGNSLVTLLCH-LFNTHGLJHHFKLDMYTLHRFLVYQEDYHSQNPYHNAHAD 180
 275 IAEI-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITYLMTLEDHYHADAVHNINHAD 333

Qy 181 VTQAMHCYKEPKLASFLPFLDIMGLLAAAADHDVHPVNVQPLIKTNHHLANLYQMS 240
 334 VVQSTHVLLSTPALEAVFTDLEILAAIFFSAIHVDHPVCSNQFLINTNSSELALMYNDS 393

Qy 241 VLENHHRSTIGMIRE 256
 Db 394 VLENHHLAVGFKLQE 409

RESULT 14
 US-08-474-379C-63
 ; Sequence 63, Application US/08474379C
 ; Patent No. 5977305
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
 ; TITLE OF INVENTION: PROCESSES
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,379C
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/206,188
 ; FILING DATE: 01-MAR-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/688,352
 ; FILING DATE: 19-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 27866/32771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: (312) 474-6300
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 673 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-474-379C-63

Db 394 VLENHHLAVGFKLQE 409

RESULT 15
 US-09-146-249A-63
 ; Sequence 63, Application US/09146249A
 ; Patent No. 606940
 ; GENERAL INFORMATION:
 ; APPLICANT: Colicelli, John J.
 ; APPLICANT: Wigler, Michael H.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; TITLE OF INVENTION: Processes
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,249A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEX: 312-474-0448
 ; FAX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 673 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-146-249A-63

Query Match Score 330.5; DB 2; Length 673;
 Best Local Similarity 37.8%; Pred. No. 3,3e-29;
 Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVRLLIS---PQRYPHASRLRGIIQAPLHLDEYLQGQHMLSKVGMWDFIPL 121
 Db 218 KEKCKRPMSQISGVKLMSSSLTNSSTRFGVTKTEQEVYLRB--LEDVNKGFLAYFR 274

Qy 122 FDRLTGNSLVTLCH-LFNTNGLIHFKLDMVTLHRLPVYQDYSQNQYHNAVHAAD 180
 Db 275 IAEI-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITMLTLEDHYADVAHNHHAAD 333

Qy 181 VTQAMHCYLIKEPKLASLFTPLD1MLGLAAAADVDHPGVNQPFLLIKTNHHLANLYQMS 240
 Db 334 VVQSTHVLLSTPALEAVETDLETLIAIFASAITHDVDPGVSNQFLINTNSSELLALMYNDSS 393

Qy 241 VLENHHRSTIGMIRE 256
 Db 394 VLENHHLAVGFKLQE 409

Search completed: March 10, 2006, 20:04:13
 Job time : 27.1463 secs

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RESULT 2
 US-10-781-181-5
 ; Sequence 5, Application US/10781181
 ; Publication No. US/20040137508A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: Fidock, Mark David
 ; TITLE OF INVENTION: Enzyme PDE xiv
 ; FILE REFERENCE: PC10315B
 ; CURRENT APPLICATION NUMBER: US/10/781,181
 ; CURRENT FILING DATE: 2004-02-18
 ; PRIOR APPLICATION NUMBER: GB 9828603.2
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/471,459
 ; PRIOR FILING DATE: 1999-12-22
 ; PRIOR APPLICATION NUMBER: GB 9922123.6
 ; PRIOR FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 450
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-781-181-5

Query Match 92.9%; Score 1430; DB 5; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.5e-142;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60
 Db 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60

Qy 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120
 Db 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120

Qy 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180
 Db 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180

Qy 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
 Db 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
 Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 4
 US-10-781-181-1
 ; Sequence 1, Application US/10781181
 ; Publication No. US/20040137508A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: Fidock, Mark David
 ; TITLE OF INVENTION: Enzyme PDE xiv
 ; FILE REFERENCE: PC10315B
 ; CURRENT APPLICATION NUMBER: US/10/781,181
 ; CURRENT FILING DATE: 2004-02-18
 ; PRIOR APPLICATION NUMBER: GB 9828603.2
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/471,459
 ; PRIOR FILING DATE: 1999-12-22
 ; PRIOR APPLICATION NUMBER: GB 9922123.6
 ; PRIOR FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-10-781-181-1

Query Match 89.4%; Score 1376; DB 4; Length 446;
 Best Local Similarity 95.1%; Pred. No. 1.3e-136;
 Matches 255; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60
 Db 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60

Qy 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120
 Db 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120

Qy 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180
 Db 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180

Qy 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
 Db 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240

RESULT 3
 US-10-204-268A-2
 ; Sequence 2, Application US/10204268A
 ; Publication No. US/2005005647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLOXEN, FRANZ-WERNER
 ; APPLICANT: HENTSCHE, BERND
 ; TITLE OF INVENTION: NEW PHOSPHODESTERASE TYPE 7B
 ; FILE REFERENCE: MERCK-2484
 ; CURRENT APPLICATION NUMBER: US/10/204-268A
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: PCT/EP01/01858
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: EP 00103655.7
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 450
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-204-268A-2

Query Match 92.9%; Score 1430; DB 5; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.5e-142;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60
 Db 1 MSCLMVERCGBILFENPDNAKCVCMGLGDIRLGQTGYAERRGSYPFDIFRLNNTYS 60

Qy 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120
 Db 61 GEIGTKKKVKRLLSFQRYPHASRLLRGITPQAPLHLDDEDYLQARHMLSKYGMWDFDIF 120

Qy 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180
 Db 121 LPDRLTNGSLVTLCLHLFNTGLHFKLDMVTLHREFLVMQEDYHSQNPFHNAHAD 180

Qy 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240
 Db 181 VTOAMHCYCLKEPKLASFLTPLDIMGLLAAAHDVDHPGVNQPFLIKTNHHLANLYONMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
 Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 5

US-10-396-414-6

; Sequence 6, Application US/10386414

; Publication No. US20040006016A1

; GENERAL INFORMATION:

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: White, David

; APPLICANT: Robison, Keith E.

; APPLICANT: Cook, William James

; APPLICANT: Meyers, Rachel E.

; APPLICANT: MacBeth, Kyle J.

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Chun, Miyoung

; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,

; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR

; FILE REFERENCE: MPI03-0210MM

; CURRENT APPLICATION NUMBER: US/10/386,414

; CURRENT FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: 09/426,282

; PRIOR FILING DATE: 1999-10-25

; PRIOR APPLICATION NUMBER: 09/668,266

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 09/339,970

; PRIOR FILING DATE: 1999-06-11

; PRIOR APPLICATION NUMBER: 09/724,599

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 09/860,193

; PRIOR FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 10/283,023

; PRIOR FILING DATE: 2002-10-29

; PRIOR APPLICATION NUMBER: 60/335,044

; PRIOR FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: 10/010,943

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: 60/254,037

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: 09/833,082

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 6

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-386-414-6

Query Match 83.1%; Score 1280; DB 4; Length 320;

Best Local Similarity 100.0%; Pred. No. 1.2e-126; Mismatches 0; Indels 0; Gaps 0;

Db 140 FKQDPLHILDEDYLGQAHRMLSKVGMWDFIDFLDRLLNGSLVTLCHLFNTGLTH 147

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 207

Db 200 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 259

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 267

Db 260 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 319

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 268

Db 320 T 320

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 268

Db 320 T 320

RESULT 6

US-10-273-517-1

; Sequence 1, Application US/10273517

; Publication No. US20030143588A1

; GENERAL INFORMATION:

; APPLICANT: THORNTON, Michael B.; DING, Li

; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.

; APPLICANT: TRIBOUTLEY, Catherine M.; LAL, Preet G.

; APPLICANT: HAFLIA, Jaya; BAUGH, Mariah R.

; APPLICANT: RAMKUMAR, Jayalakshmi; LU, Yan

; APPLICANT: CHAWLA, Narinder K.

; TITLE OF INVENTION: PHOSPHODIESTERASES

; FILE REFERENCE: PI-0136 USA

; CURRENT APPLICATION NUMBER: US/10/273,517

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: 60/241,100

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/218,234

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US01/20140

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/213,741

; PRIOR FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PERL program

; SEQ ID NO: 1

; LENGTH: 502

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1

; US-10-273-517-1

Query Match 83.1%; Score 1280; DB 4; Length 502;

Best Local Similarity 100.0%; Pred. No. 2.3e-126; Mismatches 0; Indels 0; Gaps 0;

Db 28 GDIRLRGQTGVRALERGSYPFDIDFLDRLLNGSLVTLCHLFNTGLTH 87

Qy 28 GDIRLRGQTGVRALERGSYPFDIDFLDRLLNGSLVTLCHLFNTGLTH 129

Db 80 GDIRLRGQTGVRALERGSYPFDIDFLDRLLNGSLVTLCHLFNTGLTH 147

Qy 88 IIPQAPHLIDEDYLGQAHRMLSKVGMWDFIDFLDRLLNGSLVTLCHLFNTGLTH 147

Db 140 IIPQAPHLIDEDYLGQAHRMLSKVGMWDFIDFLDRLLNGSLVTLCHLFNTGLTH 199

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 207

Db 200 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 259

Qy 208 LAAAHHDVDPHGTVNQPFLIKTNHHLANLYQNSVLEHWRSTIGMRESRLLAHLPKM 267

Db 260 LAAAHHDVDPHGTVNQPFLIKTNHHLANLYQNSVLEHWRSTIGMRESRLLAHLPKM 319

Qy 268 T 268

Db 320 T 320

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 268

Db 320 T 320

Qy 148 FKLDMDTLLHRLFVQYDTHSQNPYHNAHAADYQAMHCYLKEPKLASFPTPLDIMG 268

Db 320 T 320

; RESULT 7

US-10-386-414-4

; Sequence 4, Application US/10386414

; Publication No. US2004006016A1

; GENERAL INFORMATION:

; APPLICANT: Keppler-Libermann, Rosanna

; APPLICANT: Robison, Keith E.

; APPLICANT: White, David

; APPLICANT: Williamson, Mark W.

; APPLICANT: Cook, William James

; APPLICANT: Meyers, Rachel E.

; APPLICANT: MacBeth, Kyle J.

; APPLICANT: Carroll, Joseph M.

APPLICANT: Chun, Miyoung
 TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
 FILE REFERENCE: MP103-0210MNII
 CURRENT APPLICATION NUMBER: US/10/386, 414
 CURRENT FILING DATE: 2003-03-11
 PRIOR APPLICATION NUMBER: 09/446, 282
 PRIOR FILING DATE: 1999-10-25
 PRIOR APPLICATION NUMBER: 09/668, 266
 PRIOR FILING DATE: 2000-09-22
 PRIOR APPLICATION NUMBER: 09/330, 970
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: 09/724, 599
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 09/860, 193
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 10/583, 023
 PRIOR FILING DATE: 2002-10-29
 PRIOR APPLICATION NUMBER: 60/335, 044
 PRIOR FILING DATE: 2001-10-31
 PRIOR FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: 60/254, 037
 PRIOR FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: 09/833, 082
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-311-104-4

Query Match 63.1%; Score 1280; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.3e-16;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVAERRGSYFIDFRLNNTTYSGEIGTKKKVRLLSFORYFHASRLRG 87
 Db 80 GDIRLRGQTGVAERRGSYFIDFRLNNTTYSGEIGTKKKVRLLSFORYFHASRLRG 139

Qy 88 IIPOQAPHLDEDYLGQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIH 147
 Db 140 IIPOQAPHLDEDYLGQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIH 199

Qy 148 FKLDMDVTLHRFLVMVQEDYHSONPYHNAADVTQAMHCYLKEPKLASFLPDLIMGL 207
 Db 200 FKLDMDVTLHRFLVMVQEDYHSONPYHNAADVTQAMHCYLKEPKLASFLPDLIMGL 259

Qy 208 LAAAHDYDHPGVNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 267
 Db 260 LAAAHDYDHPGVNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 319

Qy 268 T 268
 Db 320 T 320

RESULT 9
 US-11-048-744-1
 GENERAL INFORMATION:
 Sequence 1, Application US/11048744
 Publication No. US20050164275A1
 FILE REFERENCE: PI-0136 USA
 CURRENT APPLICATION NUMBER: US/11/048-744
 CURRENT FILING DATE: 2005-02-03
 PRIOR APPLICATION NUMBER: US/10/273, 517
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: 60/241, 100
 PRIOR FILING DATE: 2000-10-16
 PRIOR APPLICATION NUMBER: 60/218, 234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US01/20140

APPLICANT: RAMKUMAR, Jayalaxmi
 LU, Yan
 APPLICANT: Chawla, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 PCT
 CURRENT APPLICATION NUMBER: US/10/311, 104
 CURRENT FILING DATE: 2003-12-12
 PRIOR APPLICATION NUMBER: PCT/US01/20140
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/213, 741
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 60/218, 234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/241, 100
 PRIOR FILING DATE: 2000-10-16
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PERL Program
 SEQ ID NO: 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
 US-10-311-104-1

Query Match 83.1%; Score 1280; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.3e-126;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVAERRGSYFIDFRLNNTTYSGEIGTKKKVRLLSFORYFHASRLRG 87
 Db 80 GDIRLRGQTGVAERRGSYFIDFRLNNTTYSGEIGTKKKVRLLSFORYFHASRLRG 139

Qy 88 IIPOQAPHLDEDYLGQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIH 147
 Db 140 IIPOQAPHLDEDYLGQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIH 199

Qy 148 FKLDMDVTLHRFLVMVQEDYHSONPYHNAADVTQAMHCYLKEPKLASFLPDLIMGL 207
 Db 200 FKLDMDVTLHRFLVMVQEDYHSONPYHNAADVTQAMHCYLKEPKLASFLPDLIMGL 259

Qy 208 LAAAHDYDHPGVNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 267
 Db 260 LAAAHDYDHPGVNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMRSRLLAHLPKEM 319

Qy 268 T 268
 Db 320 T 320

RESULT 9
 US-11-048-744-1
 GENERAL INFORMATION:
 Sequence 1, Application US/11048744
 Publication No. US20050164275A1
 FILE REFERENCE: PI-0136 USA
 CURRENT APPLICATION NUMBER: US/11/048-744
 CURRENT FILING DATE: 2005-02-03
 PRIOR APPLICATION NUMBER: US/10/273, 517
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: 60/241, 100
 PRIOR FILING DATE: 2000-10-16
 PRIOR APPLICATION NUMBER: 60/218, 234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US01/20140

APPLICANT: ARIVUZU, Chandra S.; YAO, Monique G.
 APPLICANT: THORNTON, Michael B.; DING, Li
 APPLICANT: HAFALIA, Catherine M.; LAL, Preeti G.
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: CHAWLA, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 USA
 CURRENT APPLICATION NUMBER: US/11/048-744
 CURRENT FILING DATE: 2005-02-03
 PRIOR APPLICATION NUMBER: US/10/273, 517
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: 60/241, 100
 PRIOR FILING DATE: 2000-10-16
 PRIOR APPLICATION NUMBER: 60/218, 234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US01/20140

APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: THORNTON, Michael B.
 APPLICANT: DING, Li
 APPLICANT: ARIVUZU, Chandra S.
 APPLICANT: YAO, Monique G.
 APPLICANT: TRIBBLE, Catherine M.
 APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
 APPLICANT: BAUGHN, Mariah R.

RESULT 8
 US-10-311-104-1
 GENERAL INFORMATION:
 Sequence 1, Application US/10311104
 Publication No. US20040054138A1
 FILE REFERENCE: PI-0136 USA
 CURRENT APPLICATION NUMBER: US/11/048-744
 CURRENT FILING DATE: 2005-02-03
 PRIOR APPLICATION NUMBER: US/10/273, 517
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: 60/241, 100
 PRIOR FILING DATE: 2000-10-16
 PRIOR APPLICATION NUMBER: 60/218, 234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US01/20140

PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/2113,741
 PRIOR FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PERL Program
 SEQ ID NO 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc feature
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 7476201CD1
 US-11-048-744-1

Query Match 83.1%; Score 1280; DB 6; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.3e-126;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVRABERGSYPPIDERLLNSTTYSGEIGTKKKVRLSFORFHSRLRG 87
 Db 80 GDIRLRGQTGVRABERGSYPPIDERLLNSTTYSGEIGTKKKVRLSFORFHSRLRG 139

Qy 88 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 147
 Db 140 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 199

Qy 88 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 147
 Db 140 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 199

Qy 148 FKLDMDVTLHRFLVMQEDYHSQNPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 207
 Db 200 FKLDMDVTLHRFLVMQEDYHSQNPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 259

Qy 208 LAAAHDDVDPGYNQPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 267
 Db 260 LAAAHDDVDPGYNQPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 319

Qy 268 T 268
 Db 320 T 320

RESULT 11
 US-10-204-268A-4

Qy Sequence 4, Application US/10204268A
 Db Publication No. US20050058647A1

GENERAL INFORMATION:
 APPLICANT: KLOXEN, FRANZ-WERNER
 INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
 FILE REFERENCE: MERCK-248
 CURRENT APPLICATION NUMBER: US/10/204,268A
 CURRENT FILING DATE: 2002-08-20
 PRIOR APPLICATION NUMBER: PCT/EP01/01858
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: EP 00103655.7
 PRIOR FILING DATE: 2000-02-21
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (188)
 OTHER INFORMATION: Pro or His
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (387)
 OTHER INFORMATION: Val, Ala, Asp, Glu or Gly

US-10-204-268A-4

RESULT 10
 US-11-048-068-1

Sequence 1, Application US/11048068
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: THORNTON, Michael
 APPLICANT: DING, Li
 APPLICANT: PATTERSON, Chandra
 APPLICANT: YAO, Monique G.
 APPLICANT: TRIBOUTRY, Catherine M.
 APPLICANT: LAL, Preeti
 APPLICANT: HAFALIA, April J. A.
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: RAKUMAR, Jayalaxmi
 APPLICANT: LU, Yan
 APPLICANT: WALIA, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 PCT
 CURRENT APPLICATION NUMBER: US/11/048,068
 CURRENT FILING DATE: 2005-02-02
 PRIOR FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PERL Program
 SEQ ID NO 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 7476201CD1
 US-11-048-068-1

Query Match 83.1%; Score 1280; DB 6; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.3e-126;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVRABERGSYPPIDERLLNSTTYSGEIGTKKKVRLSFORFHSRLRG 87
 Db 80 GDIRLRGQTGVRABERGSYPPIDERLLNSTTYSGEIGTKKKVRLSFORFHSRLRG 139

Qy 88 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 147
 Db 140 IIPOAFLHILDEDYLQOAHMLSKVGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIH 199

Qy 148 FKLDMDVTLHRFLVMQEDYHSQNPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 207
 Db 200 FKLDMDVTLHRFLVMQEDYHSQNPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 259

Qy 208 LAAAHDDVDPGYNQPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 267
 Db 260 LAAAHDDVDPGYNQPFLIKTNHHLANLYQNMSVLHENHWRSITGMRESRLLAHLPKEM 319

Qy 268 T 268
 Db 320 T 320

RESULT 11
 US-10-204-268A-4

Qy Sequence 4, Application US/10204268A
 Db Publication No. US20050058647A1

GENERAL INFORMATION:
 APPLICANT: KLOXEN, FRANZ-WERNER
 INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
 FILE REFERENCE: MERCK-248
 CURRENT APPLICATION NUMBER: US/10/204,268A
 CURRENT FILING DATE: 2002-08-20
 PRIOR APPLICATION NUMBER: PCT/EP01/01858
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: EP 00103655.7
 PRIOR FILING DATE: 2000-02-21
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (188)
 OTHER INFORMATION: Pro or His
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (387)
 OTHER INFORMATION: Val, Ala, Asp, Glu or Gly

US-10-204-268A-4

RESULT 10
 US-11-048-068-1

Sequence 1, Application US/11048068
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: THORNTON, Michael
 APPLICANT: DING, Li
 APPLICANT: PATTERSON, Chandra
 APPLICANT: YAO, Monique G.
 APPLICANT: TRIBOUTRY, Catherine M.
 APPLICANT: LAL, Preeti
 APPLICANT: HAFALIA, April J. A.
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: RAKUMAR, Jayalaxmi
 APPLICANT: LU, Yan
 APPLICANT: WALIA, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 PCT
 CURRENT APPLICATION NUMBER: US/11/048,068
 CURRENT FILING DATE: 2005-02-02
 PRIOR FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PERL Program
 SEQ ID NO 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 7476201CD1
 US-11-048-068-1

Query Match 74.4%; Score 1145; DB 5; Length 391;
 Best Local Similarity 99.5%; Pred. No. 3.2e-112;
 Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 RLUNSTTYSGEIGTKKKVRLSFORFHSRLRGIPQAPLHLDDEYLQOAHMLSK 111
 Db 10 RLUNSTTYSGEIGTKKKVRLSFORFHSRLRGIPQAPLHLDDEYLQOAHMLSK 69

Qy 112 VGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIHFKLDMVTLHRFLVMQEDYHSQNP 171
 Db 70 VGMWDFDIFLFDRLTNGSLVTLLCHLFNTHGLIHFKLDMVTLHRFLVMQEDYHSQNP 129

Qy 172 YHNAVHAADYTOAMHCYKLEPKLASFPTPLDIMGLAAAHDYDHPGSYNOPELIKTNNH 231
 Db 130 YHNAVHAADYTOAMHCYKLEPKLASFPTPLDIMGLAAAHDYDHPGSYNOPELIKTNNH 189

Qy 232 LANLYQMSVLHENHWRSITGMRESRLLAHLPKEMT 268

Db 190 LANLYQNMSVLENHWRSTIGMLRESRLAHLPKEMT 226
 RESULT 12
 US-10-771-833-23
 ; Sequence 23, Application US/10771833
 ; GENERAL INFORMATION:
 ; APPLICANT: MILBURN, MICHAEL V.
 ; TITLE OF INVENTION: PDEBA CRYSTAL STRUCTURE AND USES
 ; FILE REFERENCE: 03963-1106
 ; CURRENT APPLICATION NUMBER: US/10/771, 833
 ; CURRENT FILING DATE: 2004-02-03
 ; PRIOR FILING DATE: 2003-07-07
 ; PRIOR APPLICATION NUMBER: 60/444,734
 ; PRIOR FILING DATE: 2003-02-03
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO: 23
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-771-833-23

Query Match 63.6%; Score 980; DB 5; Length 335;
 Best Local Similarity 100.0%; Pred. No. 7.9e-95; Mismatches 0; Indels 0; Gaps 0;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 61 HFKLDMVTLLRFLVMQDPDYHSNPYNAVAADVTQAMCYLKEPKLASFLTPLDIMG 206
 Qy 87 GIIPQAPHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTGNSLVTLCHLFNTGLIH 146
 Db 147 HFKLDMVTLLRFLVMQDPDYHSNPYNAVAADVTQAMCYLKEPKLASFLTPLDIMG 206
 Qy 147 HFKLDMVTLLRFLVMQDPDYHSNPYNAVAADVTQAMCYLKEPKLASFLTPLDIMG 206
 Db 1 61 HFKLDMVTLLRFLVMQDPDYHSNPYNAVAADVTQAMCYLKEPKLASFLTPLDIMG 120
 Qy 87 GIIPQAPHLDDEDYLQARHMLSKVGMWDFDIFLFDRLTGNSLVTLCHLFNTGLIH 146
 Db 1 61 HFKLDMVTLLRFLVMQDPDYHSNPYNAVAADVTQAMCYLKEPKLASFLTPLDIMG 206
 Qy 207 LLAAAADHDHPGVNQPFLIKTNHLYQNMSVLENHWRSTIGMLRESRLAHLPK 266
 Db 121 LLAAAADHDHPGVNQPFLIKTNHLYQNMSVLENHWRSTIGMLRESRLAHLPK 180
 Qy 267 MT 268
 Db 181 MT 182

RESULT 14
 US-10-380-437-6
 ; Sequence 6, Application US/10380437
 ; Publication No. US20050058998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beavoc, Joseph A.
 ; APPLICANT: Soderling, Scott Haydn
 ; APPLICANT: Rascon, Ana
 ; APPLICANT: Zoragni, Roya
 ; APPLICANT: Kunz, Stefan
 ; APPLICANT: Gong, Kewei
 ; APPLICANT: Glavas, Natalie
 ; TITLE OF INVENTION: NOVEL PDES AND USES THEREOF
 ; FILE REFERENCE: 30429-3W001
 ; CURRENT APPLICATION NUMBER: US/10/380,437
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: 60/232,445
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: 60/240,500
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 6
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-380-437-6

Query Match 58.9%; Score 907; DB 5; Length 424;
 Best Local Similarity 64.6%; Pred. No. 5.9e-87; Mismatches 53; Indels 0; Gaps 0;

Db 46 QRGAIASYDSSQDTALYIRMLGDVRRSRAGFESERGSHPYIDFRIFHSQEIEVSVA 1.05
 Qy 7 ERGEITLFENPDONAKCVCMLGDIRLRGQTGYRAERGSYPFTDFRULNSTYSGEIGTK 66
 Db 106 RNIRRALLSFORTLSRSEFRGTAVSNILDDYNGQAKCMLKEVNNWFDFLFLDRLT 165
 Qy 127 NGNSLTVLLCHLFNTGLIHFKLDWTLHRLVMQDYSQNPFNAVAADVTQAMH 186
 Db 166 NGNSLVSUTFHFSLGLIUYFHDIMKLRRELVMQDYSQNPFNAVAADVTQAMH 225
 Qy 187 CYLKEPKLASFLTPLDIMG1AAAHDDHPGVNQPFLIKTNHLYQNMSVLENH 246
 Db 226 CYLKEPKLANSVTPWDILLSSTAATHDHEGVNQPFLIKTNHYLATLYKNTSVLENH 285
 Qy 247 WRSTIGMLRESRLAHLPK 266
 Db 286 WRSAVGMLRESRLAHLPK 305

Query Match 63.6%; Score 980; DB 5; Length 335;
 ; Sequence 23, Application US/10886949
 ; Publication No. US20050079548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEAN R. ARTIS
 ; APPLICANT: BOILLAG, GIDEON
 ; APPLICANT: CARD, GRAHAM
 ; APPLICANT: MARTIN, FERNANDO V.
 ; APPLICANT: MILBURN, MICHAEL V.
 ; APPLICANT: ZHANG, KAM
 ; TITLE OF INVENTION: PDEBA CRYSTAL STRUCTURE AND USES
 ; FILE REFERENCE: 03963-1108
 ; CURRENT APPLICATION NUMBER: US/10/886, 949
 ; CURRENT FILING DATE: 2004-07-07
 ; PRIOR APPLICATION NUMBER: 60/485, 627
 ; PRIOR FILING DATE: 2003-07-07
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO: 23
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-886-949-23

RESULT 15
US-10-380-437-53
Sequence 53, Application US/1080437
Publication No. US2005005898A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A
APPLICANT: Sebeck, Thomas
APPLICANT: Soderling, Scott Haydn
APPLICANT: Rascon, Ana
APPLICANT: Zoragh, Roya
APPLICANT: Kunz, Stefan
APPLICANT: Gong, Kwei
APPLICANT: Glavas, Natalie
TITLE OF INVENTION: NOVEL PDBS AND USES THEREOF
FILE REFERENCE: 30459-3W001
CURRENT APPLICATION NUMBER: US/10/380,437
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: 60/232,445
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/240,500
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NO: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 53
LENGTH: 424
TYPE: PRT
ORGANISM: Homo sapiens
US-10-380-437-53

Query Match 58.9%; Score 907; DB 5; Length 424;
Best Local Similarity 64.6%; Pred. No. 5_9e-87;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

Qy 7 ERGBILPFENPDONAKCVCMLGDIRLRCGTGVRPAERRSGTYPEDFRLLNITYSGEIGTK 66
Db 46 QRRAISYSSDQTALEYRMLGDVRVSAGFESBRGSHPYDFRLPHQSSELEVSVA 105
Qy 67 KKVKRLLSPORYFHASRLRGLIIPQAFLHLDDEYLQRGRHMLSKVGMWDFDFLFDRLT 126
Db 106 RNIRRLLSPOYLRSSRFRTGATVNSLNJLDDDGNGQAKCMLEKVGNWFDFLFDRLT 165
Qy 127 NGNSLVLVTLCHLFTNTHGLHFKLDMVTHFLMVFQDYSHSOPYNAVAADVTQAMH 186
Db 166 NGNSLVLSLTPHFLSIHLGLIEYFLIDMKLRRFLVMIQEYHSQNPYNAVAADVTQAMH 225
Qy 187 CYLKEPKLASFLLTDIMGLLAAAHHDYDHEGVNQPFLIKTNHHLANDYQNMISVLENH 246
Db 226 CYLKEPKLANSVTPDILSLIAATHDDHPEGVNQPFLIKTNHLYLATLYKNTSVLENH 285
Qy 247 WRSTIGMLRESRLLAHLPKS 266
Db 286 WRSAVGLLRESGLFSHLPPB 305

Search completed: March 10, 2006, 20:22:33
Job time : 80.0244 secs

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OM protein - protein search, using sw model

Run on: March 10, 2006, 20:19:01 ; Search time 11.3171 Seconds

(without alignment(s)
708.350 Million cell updates/sec

Title: US-10-781-181-3

Perfect score: 1540

Sequence.: 1 MSCLMVERCGHILFFNPNDQN.....GTWDDFIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:
1: /cgn2_6_ptodata/2_pubpa/_NEW_PUB_pep:
2: /cgn2_6_ptodata/2_pubpa/_US06_NEW_PUB_pep:
3: /cgn2_6_ptodata/2_pubpa/_US07_NEW_PUB_pep:
4: /cgn2_6_ptodata/2_pubpa/_PC1_NEW_PUB_pep:
5: /cgn2_6_ptodata/2_pubpa/_US05_NEW_PUB_pep:
6: /cgn2_6_ptodata/2_pubpa/_US10_NEW_PUB_pep:
7: /cgn2_6_ptodata/2_pubpa/_US11_NEW_PUB_pep:
8: /cgn2_6_ptodata/2_pubpa/_US60_NEW_PUB_pep:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best result, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1280	83.1	320	7	US-11-226-701-6	Sequence 6, Appl1
2	1280	83.1	502	7	US-11-226-701-4	Sequence 4, Appl1
3	331.5	21.5	747	6	US-10-492-835-8	Sequence 8, Appl1
4	331.5	21.5	747	6	US-10-492-835-15	Sequence 15, Appl1
5	331.5	21.5	747	6	US-10-492-835-27	Sequence 27, Appl1
6	330.5	21.5	507	7	US-11-091-018-10	Sequence 10, Appl1
7	330.5	21.5	585	7	US-11-091-018-9	Sequence 9, Appl1
8	330.5	21.5	673	7	US-11-091-018-6	Sequence 6, Appl1
9	330.5	21.5	687	7	US-11-091-018-8	Sequence 8, Appl1
10	330.5	21.5	745	7	US-11-091-018-4	Sequence 4, Appl1
11	330.5	21.5	748	6	US-10-492-835-12	Sequence 12, Appl1
12	330.5	21.5	748	6	US-10-492-835-28	Sequence 28, Appl1
13	330.5	21.5	809	7	US-11-091-018-2	Sequence 2, Appl1
14	314.5	20.4	736	7	US-11-169-041-007	Sequence 207, Appl1
15	303.5	19.7	398	7	US-11-123-893-11	Sequence 11, Appl1
16	302.5	19.6	349	7	US-11-123-893-13	Sequence 13, Appl1
17	296.5	19.3	357	7	US-11-123-893-12	Sequence 12, Appl1
18	261	16.9	769	7	US-11-072-512-2646	Sequence 266, Appl1
19	189	12.3	786	7	US-11-072-512-2344	Sequence 294, Appl1
20	185	12.0	941	6	US-10-501-035-343	Sequence 343, Appl1
21	176.5	11.5	854	6	US-10-511-657-4	Sequence 4, Appl1
22	98	6.4	968	6	US-10-501-035-219	Length: 320
23	84	5.5	635	7	US-11-096-568A-29628	Type: PRT
24	84	5.5	710	7	US-11-096-568A-29627	Organism: Homo Sapiens
25	82.5	5.4	418	7	US-11-109-156-2	US-11-226-701-6

ALIGNMENTS

RESULT 1
US-11-226-701-6

; Sequence 6, Application US/11226701
; Publication No. US20060009632A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10118 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP-103-0310MNIM
; CURRENT APPLICATION NUMBER: US/11/226,701
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: US/10/286,414
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6

US-11-226-701-4									
Query Match		Best Local Similarity		Score		DB		Length	
Matches	241; Conservative	100.0%	Pred. No.	1.3e-123;		7	502;	83.1%	Score 1280;
Matches	0; Mismatches 0;	Indels 0;	Gaps 0;			Best Local Similarity 100.0%;	Pred. No. 2.3e-123;	83.1%	Score 1280;
Y	28 GDIRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 87	Qy	83.1%;	Score 1280;	DB 7;	Length 502;			
Y	80 GDRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 139	Db	80 GDIRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 139	Qy	28 GDIRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 87	Db	80 GDIRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 139	Qy	28 GDIRLRGOTGVRAERRGSYFPIDFRLNNTTSGEIGTKKVKRLLSFORYPHASRLRG 87
Y	88 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 147	Qy	88 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 147	Db	88 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 147	Qy	88 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 147	Db	88 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 147
Y	140 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 199	Db	140 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 199	Qy	140 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 199	Db	140 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 199	Qy	140 TIPQAPLHLDEDYLQARHMLSKVGMDFDIFLFDRLTNGSLVTLCHLFNTHGLIHH 199
Y	148 FKLDMVTLHRFLVMQEDYHSQNPNPYHNAHADYTOAMHCYLTKEPKLASFLTPLDIMGL 207	Qy	148 FKLDMVTLHRFLVMQEDYHSQNPNPYHNAHADYTOAMHCYLTKEPKLASFLTPLDIMGL 207	Db	200 FKLDMVTLHRFLVMQEDYHSQNPNPYHNAHADYTOAMHCYLTKEPKLASFLTPLDIMGL 259	Qy	148 FKLDMVTLHRFLVMQEDYHSQNPNPYHNAHADYTOAMHCYLTKEPKLASFLTPLDIMGL 207	Db	200 FKLDMVTLHRFLVMQEDYHSQNPNPYHNAHADYTOAMHCYLTKEPKLASFLTPLDIMGL 259
Y	208 LAAAHDYDHPGVNQPFLLKTNHFHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 267	Qy	208 LAAAHDYDHPGVNQPFLLKTNHFHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 267	Db	260 LAAAHDYDHPGVNQPFLLKTNHFHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 319	Qy	208 LAAAHDYDHPGVNQPFLLKTNHFHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 267	Db	260 LAAAHDYDHPGVNQPFLLKTNHFHLANLYQNMSVLENHWRSTIGMLRESRLLAHLPKEM 319
Y	268 T 268	Qy	268 T 268	Db	320 T 320	Qy	268 T 268	Db	320 T 320
RESULT 2									
US-11-226-701-4									
Sequence 4 Application US/11226701									
Publication No. US20060009632A1									
GENERAL INFORMATION:									
APPLICANT: Millennium Pharmaceuticals, Inc.									
APPLICANT: Kapeller-Libermann, Rosana									
APPLICANT: Robison, Keith B.									
APPLICANT: White, David									
APPLICANT: Williamson, Mark W.									
APPLICANT: Cook, William James									
APPLICANT: Meyers, Rachel E.									
APPLICANT: MacBeth, Kyle J.									
APPLICANT: Carroll, Joseph M.									
APPLICANT: Chun, Miyoung									
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,									
FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR									
CURRENT APPLICATION NUMBER: US/11/226,701									
CURRENT FILING DATE: 2005-09-14									
PRIOR APPLICATION NUMBER: US/10/386,414									
PRIOR FILING DATE: 2003-03-11									
PRIOR APPLICATION NUMBER: 09/426,282									
PRIOR FILING DATE: 1999-10-25									
PRIOR APPLICATION NUMBER: 09/668,266									
PRIOR FILING DATE: 2001-09-22									
PRIOR APPLICATION NUMBER: 09/330,970									
PRIOR FILING DATE: 1999-06-11									
PRIOR APPLICATION NUMBER: 09/724,599									
PRIOR FILING DATE: 2000-11-28									
PRIOR APPLICATION NUMBER: 09/860,193									
PRIOR FILING DATE: 2001-05-16									
PRIOR APPLICATION NUMBER: 09/571,689									
PRIOR FILING DATE: 2000-05-16									
PRIOR APPLICATION NUMBER: 10/283,023									
PRIOR APPLICATION NUMBER: 10/335,044									
PRIOR FILING DATE: 2001-10-21									
PRIOR FILING DATE: 2002-10-29									
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PRIOR FILING DATE: 2057-10-29									
PRIOR FILING DATE: 2058-10-29									
PRIOR FILING DATE: 2059-10-29									
PRIOR FILING DATE: 2060									

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4 LENGTH: 502
TYPE: PRT ORGANISM: Homo Sapiens
RESULT 4
NUMBER 15-
US-10-442-835-15 ; Sequence 15, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION

; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS

; FILE REFERENCE: MEMORY 4 WO

; CURRENT APPLICATION NUMBER: US10/492,835

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 15

; LENGTH: 747

; TYPE: PRT

; ORGANISM: Murine sp.

; US-10-492-835-15

Query Match 21.5%; Score 331.5; DB 6; Length 747;

Best Local Similarity 37.8%; Pred. No. 8.7e-26; Indels 9; Gaps 4;

Matches 74; Conservative 35; Mismatches 78; Delins 9; Gaps 4;

Qy 66 KKKVYRLLS ---PORYFHASRLRGIIPOAFLHLDDEYLQARHMLSKVGMWDFDLFL 121

Db 293 KEKCKRPMSQISGVKKLMISSSLTNSCPRGVTEQBYLAKE--LEDVNKGGLAYER 349

Qy 122 FDRLTNGNSLVTLCH-LFNTHGJLHHFKLDMYTLLHREFVQDYHSQNPYRNAVAHD 180

Db 350 IAEL-SGNRPLTVIMHTIQERDLKTFKIPVDTLITMLEDHYDAVAYRNTHAHD 408

Qy 181 VTQAMHCYKLEPKLASFLTPLDIMIGLLAAAHDVDPGYNQPLIKTNHHLANLYQNS 240

Db 409 VVQSTHVLSTPALEAVFTDLEILAAIFASAIDVDHPGSNQFLINTNSEALMYNDSS 468

Qy 241 VLENHHRSTIGMRE 256

Db 469 VLENHHLAVGFKLQ 484

RESULT 6
US-11-091-018-10 ; Sequence 10, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345, 2010-016
; CURRENT APPLICATION NUMBER: US/11/091, 018
; PRIORITY NUMBER: PCT/US03/29906
; PRIOR APPLICATION NUMBER: 10/650, 120
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255, 120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419, 723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650, 120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067, 514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811, 352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-091-018-10

Query Match 21.5%; Score 330.5; DB 7; Length 507;
Best Local Similarity 37.8%; Pred. No. 6.6e-26;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKKVYRLLS ---PORYFHASRLRGIIPOAFLHLDDEYLQARHMLSKVGMWDFDLFL 121
Db 52 KEKCKRPMSQISGVKKLMISSSLTNSCPRGVTEQBYLAKE--LEDVNKGGLAYER 108

Qy 122 FDRLTNGNSLVTLCH-LFNTHGJLHHFKLDMYTLLHREFVQDYHSQNPYRNAVAHD 180
Db 109 IAEL-SGNRPLTVIMHTIQERDLKTFKIPVDTLITMLEDHYDAVAYRNTHAHD 167

Qy 181 VTQAMHCYKLEPKLASFLTPLDIMIGLLAAAHDVDPGYNQPLIKTNHHLANLYQNS 240
Db 168 VVQSTHVLSTPALEAVFTDLEILAAIFASAIDVDHPGSNQFLINTNSEALMYNDSS 227

Qy 241 VLENHHRSTIGMRE 256
Db 228 VLENHHLAVGFKLQ 243

RESULT 5
US-10-492-835-27 ; Sequence 27, Application US/10492835
; Publication No. US20050283660A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US10/492,835
; NUMBER OF SEQ ID NOS: 28
; CURRENT FILING DATE: 2004-04-15
; SEQ ID NO 27
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-492-835-27

Query Match 21.5%; Score 331.5; DB 6; Length 747;
Best Local Similarity 37.8%; Pred. No. 8.7e-26; Indels 9; Gaps 4;
Matches 74; Conservative 35; Mismatches 78; Delins 9; Gaps 4;

Qy 66 KKKVYRLLS ---PORYFHASRLRGIIPOAFLHLDDEYLQARHMLSKVGMWDFDLFL 121
Db 293 KEKCKRPMSQISGVKKLMISSSLTNSCPRGVTEQBYLAKE--LEDVNKGGLAYER 349

Qy 122 FDRLTNGNSLVTLCH-LFNTHGJLHHFKLDMYTLLHREFVQDYHSQNPYRNAVAHD 180
Db 350 IAEL-SGNRPLTVIMHTIQERDLKTFKIPVDTLITMLEDHYDAVAYRNTHAHD 408

Qy 181 VTQAMHCYKLEPKLASFLTPLDIMIGLLAAAHDVDPGYNQPLIKTNHHLANLYQNS 240
Db 409 VVQSTHVLSTPALEAVFTDLEILAAIFASAIDVDHPGSNQFLINTNSEALMYNDSS 468

Qy 241 VLENHHRSTIGMRE 256
Db 469 VLENHHLAVGFKLQ 484

RESULT 7
US-11-091-018-9 ; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretaarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345, 2010-016
; CURRENT APPLICATION NUMBER: US/11/091, 018
; PRIORITY NUMBER: PCT/US03/29906
; PRIOR APPLICATION NUMBER: 10/255, 120
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/067, 514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811, 352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-091-018-9

PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-091-018-9

Query Match 21.5%; Score 330.5; DB 7; Length 585;
Best Local Similarity 37.8%; Pred. No. 8e-26; Mismatches 9; Gaps 4;
Matches 74; Conservative 35; Indels 9;

Qy 66 KCKVKRLLS---FQRYFHASRLRGIIPOAQLHLDEDYLQARHMLSKVGMWDFDIFL 121
Db 130 KEKCKRPMQSISGVKKLMISSLTNSSTREGVTKTEQEVLAKE--LEDVNKGGLYFR 186

RESULT 9
US-11-091-018-8
; Sequence 8, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gregarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345_2010-016
; CURRENT APPLICATION NUMBER: US/11/091-018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8

Query Match 21.5%; Score 330.5; DB 7; Length 687;
Best Local Similarity 37.8%; Pred. No. 9.9e-26; Mismatches 78; Indels 9; Gaps 4;
Matches 74; Conservative 35; Indels 9;

Qy 66 KCKVKRLLS---FQRYFHASRLRGIIPOAQLHLDEDYLQARHMLSKVGMWDFDIFL 121
Db 232 KEKCKRPMQSISGVKKLMISSLTNSSTREGVTKTEQEVLAKE--LEDVNKGGLYFR 288

RESULT 8
US-11-091-018-6
; Sequence 6, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gregarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345_2010-016
; CURRENT APPLICATION NUMBER: US/11/091-018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-091-018-6

Query Match 21.5%; Score 330.5; DB 7; Length 673;
Best Local Similarity 37.8%; Pred. No. 9.6e-26; Mismatches 78; Indels 9; Gaps 4;

Qy 241 VLENHHRSTIGMRE 256
Db 408 VLENHHRSTIGMRE 423

RESULT 10
US-11-091-018-4

Sequence 4, Application US/11010118
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/550,120
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/711,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 745
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-11-091-018-4

Query Match 21.5%; Score 330.5; DB 7; Length 745;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Db 290 KEKKRPMQSISGYKLMSSLTNSPRFGVTEQEVYLAKE--LEDVNKGHLAYR 346

Query 66 KKVKRLLS---FQRYPHASRLRGITIQAQLHLDDEYLQARHMLSKVGMWDFDIFL 121
Db 347 IAEL-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITYLMTEDHYADVAHNIIHAD 405

Query 181 VTOAMHCYKLKEPKLASFLTPLDIMIGLJAAAHDVHPGVNOPLIKTNHHLANLYONMS 240
Db 406 VVQSTHVLLSTPALEAVFTDLEILAAFFASAITHDVHPVSNOFLINTNSEALMYNDSS 465

Query 241 VLENHWRSTIGMRE 256
Db 466 VLENHHLAVGFKLJQE 481

RESULT 11
US-10-492-835-12
; Sequence 12, Application US/10492835
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492,835
; CURRENT FILING DATE: 2004-04-15
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 12
; LENGTH: 748
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-10-492-835-12

Query Match 21.5%; Score 330.5; DB 6; Length 748;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Db 293 KEKKRPMQSISGYKLMSSLTNSPRFGVTEQEVYLAKE--LEDVNKGHLAYR 349

Query 66 KKVKRLLS---FQRYPHASRLRGITIQAQLHLDDEYLQARHMLSKVGMWDFDIFL 121
Db 350 IAEL-SGNRPLTVIMHTIQERDLIKTFKIPVDTLITYLMTEDHYADVAHNIIHAD 408

Query 181 VTOAMHCYKLKEPKLASFLTPLDIMIGLJAAAHDVHPGVNOPLIKTNHHLANLYONMS 240
Db 409 VVQSTHVLLSTPALEAVFTDLEILAAFFASAITHDVHPVSNOFLINTNSEALMYNDSS 468

RESULT 13
US-11-091-018-2
; Sequence 2, Application US/11091018
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Thorleifsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906

Query Match 21.5%; Score 330.5; DB 6; Length 748;
Best Local Similarity 37.8%; Pred. No. 1.1e-25;

PRIOR FILING DATE: 2003-09-25
 PRIOR APPLICATION NUMBER: 10/255,120
 PRIOR FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: 10/19,723
 PRIOR FILING DATE: 2003-04-18
 PRIOR APPLICATION NUMBER: 10/650,120
 PRIOR FILING DATE: 2003-08-27
 PRIOR APPLICATION NUMBER: 10/067,514
 PRIOR FILING DATE: 2002-02-04
 PRIOR APPLICATION NUMBER: 09/811,352
 NUMBER OF SEQ ID NOS: 102
 PRIOR FILING DATE: 2001-03-19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 809
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-091-018-2

Query Match 21.5%; Score 330.5; DB 7; Length 809;
 Best Local Similarity 37.8%; Pred. No. 1.e-25;
 Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

Qy 66 KKVKVRLIS---FQRYFAASRLRGITIPQAPHLIDDEYLQGARHMLSKVGMWDFDIFL 121
 Db 354 KEKKKRPMNQISGVKLMHSSSLTNSSTPRFGYKTEQBDVLAKE---LEDVWKGLHVR 410

Qy 122 FDRLTNGNSLVTLLCH-LFNTNGLIHHPKLDMYTLHFLVMQEDYHSQNQPTHNAHAAD 180
 Db 411 IAEI-SGNRPLTVIMHTFQERDLKTFPQLTPTKIPVDTLTYLMTDHYDAVHNNTHAAD 469

Qy 181 VTOAMHCVYKEPKLASFLTPDILMGLIAAAHDVDHPGVNQPLIKTNHHLANLYQNMSTLNH 240
 Db 470 VVQSTHVLLSTPALEAVPTDLELIAATPSATHDVDPGVSQFLINTNSELALMTNDSS 529

Qy 241 VLENHHRSTIGLRE 256
 Db 530 VLENHHLAVGFKLQQB 545

Query Match 19.7%; Score 303.5; DB 7; Length 398;
 Best Local Similarity 32.3%; Pred. No. 2.8e-23;
 Matches 68; Conservative 41; Mismatches 81; Indels 17; Gaps 4;

Qy 74 SFQRYPHASRLRLGIIPLQAP-----LHLDLDEYLQGARHMLSKVGMWDFDIFLFDRL 125
 Db 4 SHHHHHHSS---GLVPRGSHMSISREGVNTEDEDLAKELEDLNK--WGLNINIVAGY 56

Qy 126 TNQNSLTVLCHLFTNGLIHHPKLDMYTLHFLVMQEDYHSQNQPTHNAHAADTQAM 185
 Db 57 SHNRPTCIMYAIQERDLKTFPQLTPTKIPVDTLTYLMTDHYDSVYHNSHAADAQST 116

Qy 186 HCYLPKPKLASFLTPDILMGLIAAAHDVDHPGVNQPLIKTNHHLANLYQNMSTLNH 245
 Db 117 HVLLSTPALEAVPTDLELIAATPSATHDVDPGVSQFLINTNSELALMTNDSS 529

Query Match 20.4%; Score 314.5; DB 7; Length 736;
 Best Local Similarity 33.6%; Pred. No. 4.e-24;
 Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKVKVRLIS---FQRYFAASRLRGITIPQAPHLIDDEYLQGARHMLSKVGMWDFDIFL 121
 Db 298 KCKKQQLMTQISGVKLMHSSSLTNSSTPRFGYKTEQBDVLAKELEDLNK--WGLNINIFN 354

Qy 122 FDRLTNGNSLVTLLCH-LFNTNGLIHHPKLDMYTLHFLVMQEDYHSQNQPTHNAHAAD 181
 us-11-169-041-207

Search completed: March 10, 2006, 20:23:09
 Job time : 13.3171 secs

RESULT 15
 US-11-123-893-11
 ; Sequence 11, Application US/11123893
 ; Publication No. US2006004100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: IBRAHIM, PRABHA
 ; APPLICANT: CHO, HANNA
 ; APPLICANT: ENGLAND, BRUCE
 ; APPLICANT: GILLETT, SAM
 ; APPLICANT: ARTIS, DEAN RICHARD
 ; APPLICANT: ZUCKERMAN, REBECCA
 ; TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
 ; FILE REFERENCE: 039363-11099
 ; CURRENT APPLICATION NUMBER: US/11/123,893
 ; CURRENT FILING DATE: 2005-05-06
 ; PRIORITY APPLICATION NUMBER: 60/5569,435
 ; PRIORITY FILING DATE: 2004-05-06
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO: 11
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-123-893-11

Query Match 19.7%; Score 303.5; DB 7; Length 398;
 Best Local Similarity 32.3%; Pred. No. 2.8e-23;
 Matches 68; Conservative 41; Mismatches 81; Indels 17; Gaps 4;

Qy 74 SFQRYPHASRLRLGIIPLQAP-----LHLDLDEYLQGARHMLSKVGMWDFDIFLFDRL 125
 Db 4 SHHHHHHSS---GLVPRGSHMSISREGVNTEDEDLAKELEDLNK--WGLNINIVAGY 56

Qy 126 TNQNSLTVLCHLFTNGLIHHPKLDMYTLHFLVMQEDYHSQNQPTHNAHAADTQAM 185
 Db 57 SHNRPTCIMYAIQERDLKTFPQLTPTKIPVDTLTYLMTDHYDSVYHNSHAADAQST 116

Qy 186 HCYLPKPKLASFLTPDILMGLIAAAHDVDHPGVNQPLIKTNHHLANLYQNMSTLNH 245
 Db 117 HVLLSTPALEAVPTDLELIAATPSATHDVDPGVSQFLINTNSELALMTNDSS 529

Query Match 20.4%; Score 314.5; DB 7; Length 736;
 Best Local Similarity 33.6%; Pred. No. 4.e-24;
 Matches 71; Conservative 44; Mismatches 87; Indels 9; Gaps 3;

Qy 66 KKVKVRLIS---FQRYFAASRLRGITIPQAPHLIDDEYLQGARHMLSKVGMWDFDIFL 121
 Db 298 KCKKQQLMTQISGVKLMHSSSLTNSSTPRFGYKTEQBDVLAKELEDLNK--WGLNINIFN 354

Qy 122 FDRLTNGNSLVTLLCH-LFNTNGLIHHPKLDMYTLHFLVMQEDYHSQNQPTHNAHAAD 181

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OM protein - protein search, using sw model 1

Run on: March 10, 2006, 19:52:00 ; Search time 166.463 Seconds
(without alignments), 1187.771 Million cell updates/sec

Title: US-10-781-181-5

Perfect score: 2408

Sequence: 1 MSCLMVERCGBILFENPDQN.....PDHDHAGQGTESEREQGDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2408	100.0	450	3	AAY93569	Aay93569 Amino aci	
2	2408	100.0	450	4	AAU08675	Aau08675 Human pho	
3	2408	100.0	450	4	AGG78915	Aag78915 Human typ	
4	2401	99.7	450	8	ADP79549	Adp79549 Human pho	
5	2258	93.8	502	5	ABB09015	Abb09015 Human pho	
6	2258	93.8	502	8	ADJ58904	Adj58904 Human cyc	
7	2234	92.8	502	4	AAB36503	Aab36503 Human lon	
8	2219.5	92.2	451	3	AAY93575	Aay93575 Amino aci	
9	2192	91.0	446	3	AAY93567	Aay93567 Amino aci	
10	2166	90.0	446	3	AAY93574	Aay93574 Amino aci	
11	2165.5	89.9	445	3	AAY93573	Aay93573 Amino aci	
12	2121	88.1	437	3	AAY93572	Aay93572 Amino aci	
13	1990.5	82.7	413	3	AAY93571	Aay93571 Amino aci	
14	1865	77.5	391	4	AAU08676	Aau08676 Human pho	
15	1801	74.8	335	9	ADY50214	Ady50214 Human PDE	
16	1801	74.8	335	9	ADZ46770	Adz46770 Human PDE	
17	1430	59.4	268	3	AAY93593	Aay93593 Amino aci	
18	1430	59.4	288	3	AAY93568	Aay93568 Amino aci	
19	1425.0	59.2	456	5	AAB24510	Aab24510 Mouse PDE	
20	1419.5	58.9	482	5	ARE24531	Are24531 Human PDE	
21	1419.5	58.9	482	8	AD040842	Ad040842 Human pho	
22	1419.5	58.9	482	9	ADR46207	Adr46207 Human pho	
23	1419.5	58.9	482	9	ADY18032	Ady18032 PRO polyp	
24	1419.5	58.9	498	2	AAW00094	Aaw00094 CAMP phos	

ALIGNMENTS

RESULT 1
ID AAY93569 standard; protein; 450 AA.
XX
AC AAY93569;
XX DT 25-SEP-2000 (first entry)
XX DE Amino acid sequence of a human phosphodiesterase enzyme.
XX KW Phosphodiesterase; PDE-XIV; human; enzyme.
XX OS Homo sapiens.
XX PN EP1018559-A1.
XX PR 23-DEC-1998; 98GB-00028603.
XX PR 17-SEP-1999; 99GB-00022123.
XX PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX PI Fidock M;
XX DR WPI; 2000-433274/38.
XX DR N-PDB; AAA46651.
XX Disclosure; Page 45-47; 104pp; English.
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens in the production of antibodies against PDE-XIV and in assays to
CC identify modulators (agonists and antagonists) of PDE-XIV expression and

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	2408	100.0	450	3	AAY93569	Aay93569 Amino aci
2	2408	100.0	450	4	AAU08675	Aau08675 Human pho
3	2408	100.0	450	4	AGG78915	Aag78915 Human typ
4	2401	99.7	450	8	ADP79549	Adp79549 Human pho
5	2258	93.8	502	5	ABB09015	Abb09015 Human pho
6	2258	93.8	502	8	ADJ58904	Adj58904 Human cyc
7	2234	92.8	502	4	AAB36503	Aab36503 Human lon
8	2219.5	92.2	451	3	AAY93575	Aay93575 Amino aci
9	2192	91.0	446	3	AAY93567	Aay93567 Amino aci
10	2166	90.0	446	3	AAY93574	Aay93574 Amino aci
11	2165.5	89.9	445	3	AAY93573	Aay93573 Amino aci
12	2121	88.1	437	3	AAY93572	Aay93572 Amino aci
13	1990.5	82.7	413	3	AAY93571	Aay93571 Amino aci
14	1865	77.5	391	4	AAU08676	Aau08676 Human pho
15	1801	74.8	335	9	ADY50214	Ady50214 Human PDE
16	1801	74.8	335	9	ADZ46770	Adz46770 Human PDE
17	1430	59.4	268	3	AAY93593	Aay93593 Amino aci
18	1430	59.4	288	3	AAY93568	Aay93568 Amino aci
19	1425.0	59.2	456	5	AAB24510	Aab24510 Mouse PDE
20	1419.5	58.9	482	5	ARE24531	Are24531 Human PDE
21	1419.5	58.9	482	8	AD040842	Ad040842 Human pho
22	1419.5	58.9	482	9	ADR46207	Adr46207 Human pho
23	1419.5	58.9	482	9	ADY18032	Ady18032 PRO polyp
24	1419.5	58.9	498	2	AAW00094	Aaw00094 CAMP phos

CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
 CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
 CC gene and/or expression product may be used in the preparation of a
 CC composition for the treatment of a disorder associated with inappropriate
 CC PDE-XIV expression and/or activity to screen for agents that can
 CC modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies
 CC may also be used as diagnostic agents for detecting the presence of PDE-
 CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA))

XX

SQ Sequence 450 AA;

Query Match 100.0%; Score 2408; DB 3; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.6e-226; Mismatches 0; Gaps 0;
 Matches 450; Conservative 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGBILPENPDONAKCVCMGLDIRLRGOTGVAERGSYPPFDERLINSITYS 60
 Db 1 MSCLMVERCGBILPENPDONAKCVCMGLDIRLRGOTGVAERGSYPPFDERLINSITYS 60
 Qy 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Db 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Qy 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Db 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Qy 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Db 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Qy 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Db 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Qy 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Db 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Qy 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Db 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Qy 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450
 Db 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450

RESULT 2
 AAU08675 standard; protein; 450 AA.

XX

AC AAU08675;

XX DT 18-DEC-2001 (first entry)

XX DE Human phosphodiesterase type 7B #1.

XX KW Human; phosphodiesterase type 7B; cardiovascular disease; asthma;

KW allergy; inflammatory disease; immune related disorder; cardiovascular;
 KW antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.

XX OS Homo sapiens.

XX PN WO200165940-A2.

XX PD 30-AUG-2001.

XX PF 20-FEB-2001; 2001WO-EP001855.

XX PR 21-FEB-2000; 2000EP-00103655.

XX

PA (MERK) MERCK PATENT GMBH.

XX PI Kluxen F, Hentsch B;

XX DR WPI; 2001-570636/64.

XX N-PSDB; AAS13248.

XX PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
 PT diagnosing and treating, e.g. asthma, inflammation and allergies.

XX SQ Claim 1; Page 36-37; 40pp; English.

XX PS The invention relates to a novel human Phosphodiesterase type 7B

CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
 CC acid may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
 CC example, The protein and nucleic acid may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P7B by expressing
 CC inactive proteins or to supplement the patients own production of P7B.CC The nucleic acids may be used to produce P7B polypeptides, by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. The nucleic acid and its complements may also be used as DNA
 CC probes in diagnostic assays to detect and quantify the presence of
 CC similar nucleic acids in samples, and therefore which patients may be in
 CC need of restorative therapy. The P7B polypeptides may also be used as
 CC antigens in the production of antibodies against P7B and in assays to
 CC identify modulators of it's expression and activity. The anti-P7B
 CC antibodies and antagonists may also be used to down regulate expression
 CC and activity. The anti-P7B antibodies may also be used as diagnostic
 CC agents for detecting the presence of P7B in samples (e.g., by enzyme
 CC linked immunoassay (ELISA)). Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include, for example
 CC cardiovascular disease, asthma, allergy, inflammation, and immune-related
 CC disorders. The present sequence represents a human phosphodiesterase 7B

XX SQ Sequence 450 AA;

XX Query Match 100.0%; Score 2408; DB 4; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.6e-226;
 Matches 450; Conservative 0; Indels 0; Gaps 0;Qy 1 MSCIMVERCGBILPENPDONAKCVCMGLDIRLRGOTGVAERGSYPPFDERLINSITYS 60
 Db 1 MSCIMVERCGBILPENPDONAKCVCMGLDIRLRGOTGVAERGSYPPFDERLINSITYS 60
 Qy 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Db 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Qy 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Db 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Qy 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Db 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Qy 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Db 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Qy 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Db 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Qy 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Db 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Qy 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450
 Db 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450Qy 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Db 61 GEIGTKKKVRLLSFQRYPHASRLLRGIPQAPHLIDDDYLQARHMLSKVGMWDFDIF 120
 Qy 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Db 121 LFDRLTNGSLVTLCHLFNTTHGLJHHFPLDMTLLHRFLYMQDYHSNPNYHNAHAAD 180
 Qy 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Db 181 VTOAMHCYLKPKLASFLPFLDIMGLLAAAHDYDHPGYNQPLKITHFLANLYQMS 240
 Qy 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Db 241 VLENHHWRSTIGMRRESRLIAHLPKEMTODIEEQQLSLLATDINRQNEFLTRLKAHN 300
 Qy 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Db 301 KDLRLEDADQDHFMQIAALKCADICNPCTIWEMSKWSKWSERVICEFYROGELEOKFELIS 360
 Qy 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Db 361 PLCNQQKDSIPIQIGMSYIPELFREWAHTFTNSTLSENMGLHLANKIAQKSSLPRQ 420
 Qy 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450
 Db 421 HRSRGSSGGSPDHAGQTESEEQGDSP 450

RESULT 3 ID AAG78915 XX AAG78915 standard; protein; 450 AA.	Qy 421 HRSRSGSGPDPDHAGCTESEBQBGDSP 450 Db 421 HRSRSGSGPDPDHAGCTESEBQBGDSP 450
XX DT 19-DEC-2001 (first entry)	RESULT 4 AC ADP79549 standard; protein; 450 AA. AC ADP79549; XX AC ADP79549; XX DT 04-NOV-2004 (first entry) XX Human phosphodiesterase 7B nucleotide sequence. XX DE Human; phosphodiesterase 7B; PDE7b; cardiovascular-Gen.; CNS-Gen.; gene therapy; XX KW synaecological; haemostatic; respiratory-Gen.; cytostatic; gene therapy; XX OS Homo sapiens. XX PN JP2001238680-A. XX PD 04-SEP-2001. XX PP 03-MAR-2000; 20000JP-00058159. XX PR 03-MAR-2000; 20000JP-00058159. XX PA (TANA) TANABE SEIYAKU CO. XX WPI; 2001-610057/70. XX DR N-PSDB; AAI70009. XX PT New phosphodiesterase for use in the development of inhibitors of high selectivity and drugs of low side effect. XX CC The present sequence is the protein sequence for human type 7B phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the development of inhibitors of high selectivity and drugs of low side effects. XX PS Claim 2; Page 12-14; 18pp; Japanese. XX CC The present sequence is that of human phosphodiesterase 7b (PDE7b), an enzyme regulating intracellular levels of cAMP and cGMP. The invention relates to novel disease associations of PDE7b polynucleotides and polypeptides. It also relates to novel methods of screening for therapeutic agents for the treatment of cardiovascular diseases, disorders of the peripheral and central nervous system, reproduction, urological, hematological, respiratory system or cancer diseases, comprises contacting a test compound with a phosphodiesterase 7b. XX SQ Sequence 450 AA;
XX	Query Match Score 2408; DB 4; Length 450; Best Local Similarity 100.0%; Pred. No. 1.6e-226; Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSCLMYVERCGHILFENPDQNAKCVMLGDRQGKGVRERRGYPFDFLRLNSTTS 60 Db 1 MSCLMYVERCGHILFENPDQNAKCVMLGDRQGKGVRERRGYPFDFLRLNSTTS 60	CC The present sequence is that of human phosphodiesterase 7b (PDE7b), an enzyme regulating intracellular levels of cAMP and cGMP. The invention relates to novel disease associations of PDE7b polynucleotides and polypeptides. It also relates to novel methods of screening for therapeutic agents for the treatment of cardiovascular diseases, disorders of the peripheral and central nervous system, reproduction, urological, hematological diseases, disorders of the respiratory system and cancer. PDE7b polynucleotides, polypeptides and antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used in the treatment or diagnosis of these diseases and disorders. CC Sequence 450 AA;
Qy 61 GBIGTRKKKVRLLSFORYFHASRLURGIIPQAPLHDIDYLQQRHMLSKVGWDFDIF 120 Db 61 GBIGTRKKKVRLLSFORYFHASRLURGIIPQAPLHDIDYLQQRHMLSKVGWDFDIF 120	CC Disclosure; SEQ ID NO 2; 128pp; English. CC DR; ADP79548.
Qy 121 LFDRLTNGSLVLLCHLNFTHGLTHFKLDMVTHRELIYMQEDYHSQNPYNAVAHAAD 180 Db 121 LFDRLTNGSLVLLCHLNFTHGLTHFKLDMVTHRELIYMQEDYHSQNPYNAVAHAAD 180	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 181 VTQAMHCKYKEPKLASFLTPDIMIGLLAAAHDYDHPGYNQPFLLKTHNLANYQNS 240 Db 181 VTQAMHCKYKEPKLASFLTPDIMIGLLAAAHDYDHPGYNQPFLLKTHNLANYQNS 240	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 241 VLENHHWRSITGMRESRLIAHLPKEMTQDIEQQLGSLLATDINRQBFTRLKAHLIN 300 Db 241 VLENHHWRSITGMRESRLIAHLPKEMTQDIEQQLGSLLATDINRQBFTRLKAHLIN 300	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 301 KDLRLEDAQDRHFMQQLAKCADICNPRIWEMSKOWSERVCEPYTQGQEOKPELEIS 360 Db 301 KDLRLEDAQDRHFMQQLAKCADICNPRIWEMSKOWSERVCEPYTQGQEOKPELEIS 360	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 361 PLCNQQDSDPSIQTGMSYIVEPLFREWIAHTGNSTLSSEMLGHLAHKQAWKSLLPRQ 420 Db 361 PLCNQQDSDPSIQTGMSYIVEPLFREWIAHTGNSTLSSEMLGHLAHKQAWKSLLPRQ 420	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 421 HRSRSGSGPDPDHAGCTESEBQBGDSP 450 Db 421 HRSRSGSGPDPDHAGCTESEBQBGDSP 450	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 99.7%; Score 2401; DB 8; Length 450; Best Local Similarity 99.8%; Pred. No. 7.6e-226; Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 1 MSCLMVERCGEILFENPDQNAKCVMLGDRQGKGVRERRGYPFDFLRLNSTTS 60 Db 1 MSCLMVERCGEILFENPDQNAKCVMLGDRQGKGVRERRGYPFDFLRLNSTTS 60	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 61 GEIGTRKKKVRLLSFORYFHASRLURGIIPQAPLHDIDYLQQRHMLSKVGWDFDIF 120 Db 61 GEIGTRKKKVRLLSFORYFHASRLURGIIPQAPLHDIDYLQQRHMLSKVGWDFDIF 120	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 121 LFDRLTNGSLVLLCHLNFTHGLTHFKLDMVTHRELIYMQEDYHSQNPYNAVAHAAD 180 Db 121 LFDRLTNGSLVLLCHLNFTHGLTHFKLDMVTHRELIYMQEDYHSQNPYNAVAHAAD 180	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 181 VTQAMHCKYKEPKLASFLTPDIMIGLLAAAHDYDHPGYNQPFLLKTHNLANYQNS 240 Db 181 VTQAMHCKYKEPKLASFLTPDIMIGLLAAAHDYDHPGYNQPFLLKTHNLANYQNS 240	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 241 VLENHHWRSITGMRESRLIAHLPKEMTQDIEQQLGSLLATDINRQBFTRLKAHLIN 300 Db 241 VLENHHWRSITGMRESRLIAHLPKEMTQDIEQQLGSLLATDINRQBFTRLKAHLIN 300	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 301 KDLRLEDAQDRHFMQQLAKCADICNPRIWEMSKOWSERVCEPYTQGQEOKPELEIS 360 Db 301 KDLRLEDAQDRHFMQQLAKCADICNPRIWEMSKOWSERVCEPYTQGQEOKPELEIS 360	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.
Qy 361 PLCNQQDSDPSIQTGMSYIVEPLFREWIAHTGNSTLSSEMLGHLAHKQAWKSLLPRQ 420 Db 361 PLCNQQDSDPSIQTGMSYIVEPLFREWIAHTGNSTLSSEMLGHLAHKQAWKSLLPRQ 420	CC PT XX PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX PR 13-NOV-2002; 2002EP-00025502. XX DR 2004-440631/41. XX DR N-PSDB; ADP79548.

Qy	181 VTOAMHCYKLKEPKLASFITPLDIMIGLLAAAHDVDPGYNOPPLIKTNTHHLANLYQMS	240	CC disorders. The polynucleotides are useful for creating humanised animals
Db	181 VTOAMHCYKLKEPKLASFITPLDIMIGLLAAAHDVDPGYNOPPLIKTNTHHLANLYQMS	240	CC or transgenic animals to model human disease and to detect and quantify
Qy	241 VLENHWRSTIGMRESRLAHLPKEMTDIEBQQLSLLATDINRQNFEFLTRKALHN	300	CC gene expression in biopsied tissues in which expression of HPDE is
Db	241 VLENHWRSTIGMRESRLAHLPKEMTDIEBQQLSLLATDINRQNFEFLTRKALHN	300	CC correlated with disease. HPDE, its fragments and antibodies specific for
Qy	301 KDLRLEDADQDRHFMQLQIALKCADCINCPRIWEMSKOWSERVCEFYROGEELEOKFELIS	360	CC HPDE are useful as elements on a microarray which is useful to monitor or
Db	301 KDLRLEDADQDRHFMQLQIALKCADCINCPRIWEMSKOWSERVCEFYROGEELEOKFELIS	360	CC measure protein-protein interactions, drug-target interactions and gene
Qy	361 PLCNQKQDSIPTSIQGMSTIVEPLFRENAHTGENSTLSENMIGLHLAINKAOKSLLPRQ	420	CC expression profiles. This sequence represents HPDE-1
Db	361 PLCNQKQDSIPTSIQGMSTIVEPLFRENAHTGENSTLSENMIGLHLAINKAOKSLLPRQ	420	XX
Qy	421 HRSRGSSGGSPDHAGQGTSESEQGDSP	450	Sequence 502 AA:
Db	421 HRSRGSSGGSPDHAGQGTSESEQGDSP	450	Query Match 93.8%; Score 2258; DB 5; Length 502;
Qy	421 HRSRGSSGGSPDHAGQGTSESEQGDSP	450	Best Local Similarity 100.0%; Pred. No. 9e-212;
Db	421 HRSRGSSGGSPDHAGQGTSESEQGDSP	450	Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 5			Oy 28 GDIRLRGOTGVRAERGSYPFDIFRLLNISTTSGEIGTKKKYKRLSFORYFHASRLJRG 87
ID ABB09005	ABB09005 standard: protein; 502 AA.		Db 80 GDIRLRGOTGVRAERGSYPFDIFRLLNISTTSGEIGTKKKYKRLSFORYFHASRLJRG 139
XX			Qy 88 IIPOAPLHILDEDLYLQARHMLSKVGMNDFDIFLFDRLTNGNSLVTLCHLFNTGLIH 147
AC ABB09005;			Db 140 IIPOAPLHILDEDLYLQARHMLSKVGMNDFDIFLFDRLTNGNSLVTLCHLFNTGLIH 199
XX			Qy 148 FKUDMDVTLHRFLYMQEDYHSQNPYHNAHAADVTQAMHCYLKPEPKLASFLPDLIMJL 207
DT 23-MAY-2002	(First entry)		Db 200 FKUDMDVTLHRFLYMQEDYHSQNPYHNAHAADVTQAMHCYLKPEPKLASFLPDLIMJL 259
XX			Qy 208 LAAAADYDHPGYNOPLJKTNNHHLANLYQNNSVLNENHWRSTIGMRESRLIAHLPKEM 267
DB Human phosphodiesterase-1.			Db 260 LAAAADYDHPGYNQPLJKTNNHHLANLYQNNSVLNENHWRSTIGMRESRLIAHLPKEM 319
XX			Qy 268 TQDIEQQGLSLTLATDINRQNFBFLTRKALHLINKDLEDAODRFHMQLIAKLCADICNP 327
KW HPDE; human phosphodiesterase; cyclic nucleotide phosphodiesterase;			Db 320 TQDIEQQGLSLTLATDINRQNFBFLTRKALHLINKDLEDAODRFHMQLIAKLCADICNP 379
KW antiinflammatory; neuroprotective; cytosstatic; antianaemic;			Qy 328 CRIWEMSKOWSERVICEFYROGEELEOKFELISPLCNQKQDSIPTSIQGMSTIVEPLFR 387
KW immunosuppressive; HIV; cardiovascular disorder; cytostatic; antianaemic;			Db 360 CRIWEMSKOWSERVICEFYROGEELEOKFELISPLCNQKQDSIPTSIQGMSTIVEPLFR 439
KW gene therapy; transgene; enzyme.			Qy 388 EWAHFITGNSTLSENMGLHLAINKAOKNSLLPROHRSRGSSGSPDHAGQGTSEBBQEG 447
XX			Db 440 EWAHFITGNSTLSENMGLHLAINKAOKNSLLPROHRSRGSSGSPDHAGQGTSEBBQEG 499
OS Homo sapiens.			Qy 448 DSP 450
XX			Db 500 DSP 502
WO200198471-A2.			RESULT 6
XX			ADJ58904
PD 27-DEC-2001.			ID ADJ58904 standard; protein; 502 AA.
XX			XX ADJ58904;
DB 21-JUN-2001; 2001WO-US020140.			XX DT 05-MAY-2004 (first entry)
XX			XX DE Human cyclic nucleotide phosphodiesterase protein #1.
PR 22-JUN-2000; 2000US-0213741D.			XX KW 2785; 22025; 27420; 17906; 16319; 55092; 1028; cancer;
PR 14-JUL-2000; 2000US-0218234P.			XX KW cellular proliferation; cellular differentiation; immune disorder;
PR 16-OCT-2000; 2000US-0241100P.			XX KW cardiovascular disorder; endothelial cell disorder; haemopoietic disorder; blood vessel disorder; brain disorder; pain;
XX			XX KW metabolic disorder; liver disorder; platelet disorder; gene therapy;
PA (INCYTE GENOMICS INC.			XX KW human; cyclic; enzyme.
XX			XX Homo sapiens.
PI Thornton M, Ding L, Patterson C, Yao MG, Tribouley CM, Lal P;			OS
PI Natalia AJA, Baughn MR, Ramkumar J, Lu Y, Walla NK;			XX
XX			XX US200406016-A1.
DR WPI: 2002-147799/19.			XX PD 08-JAN-2004.
DR N-PSDB; ABA99136.			XX PF 11-MAR-2003; 2003US-00386414.
XX			XX PR 11-JUN-1999; 99US-00333970.
PT Novel human phosphodiesterase polypeptides and polynucleotides for			
PT diagnosing, preventing and treating eye, neurological, cardiovascular,			
PT cell proliferative and autoimmune/inflammatory disorders.			
PT Claim 1; Page 97-98; 105pp; English.			
CC This invention relates to isolated human phosphodiesterase polypeptides			
CC which are antiinflammatory, neuroprotective, cytostatic,			
CC antihaemopoietic, immunosuppressive and anti-HIV in their action. The			
CC polypeptides are useful for screening a compound for effectiveness as an			
CC agonist or antagonist of the protein. The identified agonist, antagonist			
CC and protein are useful for treating a disease or condition associated			
CC with decreased or overexpression of functional HPDE in a patient. The			
CC proteins are useful in preparing monoclonal or monoclonal antibodies by			
CC hybrida technology. They are also useful in the treatment and			
CC prevention of eye, neurological, cardiovascular, cell proliferative and			
CC autoimmune and inflammatory disorders, metabolic disorders and mental			

PR 25-OCT-1999; 99US-00426282.
 PR 16-MAY-2000; 2000US-00571689.
 PR 22-SEP-2000; 2000US-00668266.
 PR 28-NOV-2000; 2000US-00724599.
 PR 07-DEC-2000; 2000US-0254037P.
 PR 10-APR-2001; 2001US-00833082.
 PR 16-MAY-2001; 2001US-00860193.
 PR 31-OCT-2001; 2001US-0355044P.
 PR 06-DEC-2001; 2001US-00010943.
 PR 29-OCT-2002; 2002US-00283023.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Kappeler-Libermann R, White D, Robison KB, Macbeth KJ, Carroll JM;
 PI Cook WJ, Meyers RE, Chun M, Williamson MJ;
 XX WPI: 2004-081738/08.
 DR N-PSDB; ADJ58903.
 XX New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecules, useful for diagnosing or treating cancer, pain, or immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic and liver disorders.
 XX Claim 4: SEQ ID NO 4; 245pp; English.
 XX The present invention relates to an isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for diagnosing or treating cancer or aberrant cellular proliferation and/or differentiation, immune disorders, heart disorders, cardiovascular disorders including endothelial cell disorders, haematopoietic disorders, blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders and platelet disorders. The invention is also useful in gene therapy. The present sequence is human cyclic nucleotide phosphodiesterase.
 XX Sequence 502 AA;

Query Match 93.8%; Score 2258; DB 8; Length 502;
 Best Local Similarity 100.0%; Pred. No. 9e-212;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGQTGVRABRGSSPFIDPRLINSTTSGBIGMKVKRLLSFRYFFASRLRG 87
 Db 80 GDIRLRGQTGVRABRGSSPFIDPRLINSTTSGBIGMKVKRLLSFRYFFASRLRG 139
 Qy 88 IIPOAFLHLDDEDYLGQARHMLSKVGMWDFDIFLFDRLTNSLVTLCHLFNTHGLIH 147
 Db 140 IIPOAFLHLDDEDYLGQARHMLSKVGMWDFDIFLFDRLTNSLVTLCHLFNTHGLIH 199
 Qy 148 FKLDMDVTLHRFLVNVQEDHTSQQNPYHNAADYVQAMCYCLEPKLASFLTDIMLG 207
 Db 200 FKLDMDVTLHRFLVNVQEDHTSQQNPYHNAADYVQAMCYCLEPKLASFLTDIMLG 259
 Qy 208 LAAAHDDVHPGYNQPLFLIKTNHHLANLYQNMSTLENHWRSTGMURSERLIAHLPKEM 267
 Db 260 LAAAHDDVHPGYNQPLFLIKTNHHLANLYQNMSTLENHWRSTGMURSERLIAHLPKEM 319

Query Match 92.8%; Score 2234; DB 4; Length 502;
 Best Local Similarity 99.1%; Pred. No. 2e-209;
 Matches 419; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 28 GDTRLRGQTGVRABRGSSPFIDPRLINSTTSGBIGTKKRYKRLSFRYFFASRLRG 87
 Db 80 GDTRLRGQTGVRABRGSSPFIDPRLINSTTSGBIGTKKRYKRLSFRYFFASRLRG 139
 Qy 388 CTRWEMSKQWSERVICEEFTRQGELEQKPFLEISPLCNCQKDSTSPIQIGFMSVIVEPLFR 439
 Db 320 TDRQEQLSSSLILATDINRNEFLTRKLHANKDLRFLDAQRHFMQLQALKCADICNP 379
 Qy 328 CRIVEMSKQWSERVICEEFTRQGELEQKPFLEISPLCNCQKDSTSPIQIGFMSVIVEPLFR 387
 Db 380 CTRWEMSKQWSERVICEEFTRQGELEQKPFLEISPLCNCQKDSTSPIQIGFMSVIVEPLFR 447
 Qy 388 EWAHTGNSTLSENNLGHIAHNKAQWSLSPRGRSGSPDHAGQTESEBEG 447
 Db 440 EWAHTGNSTLSENNLGHIAHNKAQWSLSPRGRSGSPDHAGQTESEBEG 499
 Qy 448 DSP 450
 Db 500 DSP 502

Db	61	GBIGPKKKVRLSQTQYFAASRLRGLTQAPHLIDDEYLQGARHMLSKVGKWDFFDFP	120
Qy	121	LFDRLTNGNSLVTLLCHLFTHGLIHHFLDMDVTHRFLYMVOQDYHSQNPYNAHAAD	180
Db	121	LFDRLTNGNSLVTLLCHLFTHGLIHHFLDMDVTHRFLYMVOQDYHSQNPYNAHAAD	180
Qy	181	VTOQAHCYLKEPKLASFPLTDIMIGLAAAADYDHPGYNQPFLLIKTNHHLANLYQNS	240
Db	181	VTOQAHCYLKEPKLASFPLTDIMIGLAAAADYDHPGYNQPFLLIKTNHHLANLYQNS	240
Qy	241	VLENHFWRSITGMRESRLLAHLPKEMTQDEQQLSSLILATDINQNLTRLKAHIN	300
Db	241	VLENHFWRSITGMRESRLLAHLPKEMTQDEQQLSSLILATDINQNLTRLKAHIN	300
Qy	301	KDLRLEDAQDRHFMQLIAALKCADICNPRCWMSQWNSERVICEEYRQGLEQKFELIS	360
Db	301	KDLRLEXXQDRHFMQLIAALKCADICNPRCWMSQWNSERVICEEYRQGLEQKFELIS	360
Qy	361	PLCNQKQDSIPSQIIGEMSYIVEPLFREWAHTGNSTLSERNMLGHLAHNAQWKSLLPQ	420
Db	361	PLCNQKQDSIPSQIIGEMSYIVEPLFREWAHTGNSTLSERNMLGHLAHNAQWKSLLXQ	420
Qy	421	HRSRSSSSGPDDHAGQTESEEQ- EGASP 450	
Db	421	HXRGSSSGPDDHAGXXXEQTEGKXP 451	
RESULT 9			
	AAV93567	AAV93567 standard; protein; 446 AA.	
	AAV93567;		
	25-SEP-2000	(first entry)	
		Amino acid sequence of a murine phosphodiesterase enzyme.	
		Phosphodiesterase; PDE-XIV; murine; enzyme.	
		Mus sp.	
		EP1018559-A1.	
		12-TUL-2000.	
		09-NOV-1999; 99EP-00308902.	
		23-DEC-1998; 98GB-00028603.	
		17-SEP-1999; 99GB-00022123.	
		(PFIZ) PFIZER LTD.	
		(PFIZ) PFIZER INC.	
		Fidock M;	
		WPI; 2000-433274/38.	
		N-PSDB; AAA46649.	
		Disclosure; Page 39-41; 104pp; English.	
		The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polymucotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as	
CC	antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antigens may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))		
CC	Sequence 446 AA;		
CC	SQ		
CC	Query Match 91.0%; Score 2192; DB 3; Length 446;		
CC	Best Local Similarity 91.6%; Pred. No. 2-2e-205;		
CC	Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2		
CC	Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2		
CC	Query 1 MSCLMVERCGBILFNPNDQNQAKCVMLGDITLRGGTGVRAERGGYPFIDPRLNNNTTYS 60		
CC	Db 1 MSCLMVERCGBILFNPNDQNQAKCVMLGDITLRGGTGVRAERGGYPFIDPRLNNNTTYS 60		
CC	Query 61 GEIGTKKKVYKRLLSFORYFHASRLRGITIPQAPIHLILDEDYLQGARHMLSKVGMDDFIF 120		
CC	Db 61 GEIGTKKKVYKRLLSFORYFHASRLRGITIPQAPIHLILDEDYLQGARHMLSKVGMDDFIF 120		
CC	Query 121 LFDRLTNGSLVTLCHLFNTHGLFPLDMVQEDYHGPYNAVAHAAD 180		
CC	Db 121 LFDRLTNGSLVTLCHLFNTHGLFPLDMVQEDYHGPYNAVAHAAD 180		
CC	Query 181 VTOQAHCYLKEPKLASFPLTDIMGLLAAAADYDHPGYNQPFLLIKTNHHLANLYQNMS 240		
CC	Db 181 VTOQAHCYLKEPKLASFPLTDIMGLLAAAADYDHPGYNQPFLLIKTNHHLANLYQNMS 240		
CC	Query 241 VLENHFWRSITGMRESRLLAHLPKEMTQDEQQLSSLILATDINRNEFLTRLKAHIN 300		
CC	Db 241 VLENHFWRSITGMRESRLLAHLPKEMTQDEQQLSSLILATDINRNEFLTRLKAHIN 300		
CC	Query 301 KDLRLEDAQDRHFMQLIAALKCADICNPRCWMSQWNSERVICEEYRQGLEQKFELIS 360		
CC	Db 301 KDLRLEDAQDRHFMQLIAALKCADICNPRCWMSQWNSERVICEEYRQGLEQKFELIS 360		
CC	Query 361 PLCNQKQDSIPSQIIGEMSYIVEPLFREWAHTGNSTLSERNMLGHLAHNAQWKSLLPQ		
CC	Db 361 PLCNQKQDSIPSQIIGEMSYIVEPLFREWAHTGNSTLSERNMLGHLAHNAQWKSLLPQ		
CC	Query 421 HRSRGSSSGPDDHAGQTESEEQ- EGASP 450		
CC	Db 421 HRRRSGSGPDDHAGQTESEEQ- EGASP 450		
CC	RESULT 10		
CC	AYA33574		
CC	ID AYA33574 standard; protein; 446 AA.		
CC	XX		
CC	XX		
CC	AC AYA33574;		
CC	XX		
CC	DT 25-SEP-2000 (first entry)		
CC	XX		
CC	XX		
CC	DB Amino acid sequence of a phosphodiesterase enzyme.		
CC	KW Phosphodiesterase; PDE-XIV; enzyme.		
CC	XX		
CC	OS Synthetic.		
CC	XX		
CC	FH * Location/Qualifiers		
CC	FT Misc-difference 12 /label= Val, Ile		
CC	FT Misc-difference 16 /label= Ser, Asn		
CC	FT Misc-difference 18 /label= Glu, Asp		
CC	FT Misc-difference 20 /label=		

FT	Misc-difference 21	/label= Ser, Val, Asn, Ala	PT useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.
FT	Misc-difference 30	/label= Ser, Val, Asn, Ala	PT Disclosure; Page 70-72; 10pp; English.
FT	Misc-difference 39	/label= Val, Ile	XX
FT	Misc-difference 56	/label= Pro, Arg	CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
FT	Misc-difference 59	/label= His, Tyr	CC
FT	Misc-difference 114	/label= Thr, Met	CC
FT	Misc-difference 141	/label= Ser, Thr	CC
FT	Misc-difference 168	/label= Gly, His, Ser, Gln	CC
FT	Misc-difference 169	/label= Gly, His, Ser, Gln	CC
FT	Misc-difference 307	/label= Asp, Ala, Asn, Val	CC
FT	Misc-difference 308	/label= Asp, Ala, Asn, Val	CC
FT	Misc-difference 350	/label= Glu, Asp	CC
FT	Misc-difference 379	/label= Ser, Thr	CC
FT	Misc-difference 391	/label= His, Arg	XX
FT	Misc-difference 404	/label= Gly, Ser	Sequence 446 AA:
FT	Misc-difference 418	/label= Pro, Arg, Ser, Asn	Query Match 90.0%; Score 2166; DB 3; Length 446;
FT	Misc-difference 419	/label= Pro, Arg, Ser, Asn	Best Local Similarity 91.6%; Pred. No. 7, 8e-203;
FT	Misc-difference 423	/label= Ser, Arg	Matches 413; Conservative 0; Mismatches 32; Indels 6; Gaps 2;
FT	Misc-difference 430	/label= His, Leu	Qy 1 MSCIMVERCGEILFENPDONAKCVCMLGDIRLURGOTGVYRAERRSYPPIDFRILLNSTTYS 60
FT	Misc-difference 433	/label= Gln, Gly, Thr, Pro, Ala	Db 1 MSCIMVERCGEILFEXPXQXXCVCMLGDXURGQTGXAAERRSYPPIDFRILLNXTX 60
FT	Misc-difference 434	/label= Gln, Gly, Thr, Pro, Ala	Qy 61 GEIGTKEKVKRLLSFQRYFHASRLLRGITIPQAPLHILDEDYLQGQAREHMLSKVGMWDFDF 120
FT	Misc-difference 435	/label= Gln, Gly, Thr, Pro, Ala	Db 61 GEIGTKEKVKRLLSFQYFHASRLLRGITIPQAPLHILDEDYLQGQAREHMLSKVGMWDFDF 120
FT	Misc-difference 437	/label= Ser, Glu, Thr, Leu	Qy 121 LFPLRLTGNSLYTLCHLFNTNGLIHFHKFLDMVTLLRFLVNQEDTHSQNPYHNAVHAAD 180
FT	Misc-difference 438	/label= Ser, Glu, Thr, Leu	Db 121 LFPLRLTGNSLYTLCHLFNTNGLIHFHKFLDMVTLLRFLVNQEDTHSQNPYHNAVHAAD 180
FT	Misc-difference 441	/note= "optionally absent"	Qy 181 VTOAMHCKYLKEPKLASFITPLDILMGLIIAAAHHDVHPGVNQPLFLIKTNHHHLANLYQNM 240
FT	Misc-difference 444		Db 181 VTOAMHCKYLKEPKLASFITPLDILMGLIIAAAHHDVHPGVNQPLFLIKTNHHHLANLYQNM 240
FT	Misc-difference 445	/label= Ser, Ala, Thr	Qy 241 VLENHHRSTIGMRESRLLAHLPKEMTQDIEQQLGSLLATDINRONEFLTRKAHLHN 300
XX	EP1018559-A1.		Db 241 VLENHHRSTIGMRESRLLAHLPKEMTQDIEQQLGSLLATDINRONEFLTRKAHLHN 300
XX	12-JUL-2000.		Qy 301 KDLRLEDAQDRHFMQLQALKCADICINPCRIMEMSKQMSERVICEEFYRQGELBQKFELIS 360
XX	09-NOV-1999;		Db 301 KDLRLEXQDRHFMQLQALKCADICINPCRIMEMSKQMSERVICEEFYRQGELBQKFELIS 360
XX	23-DEC-1998;	98GB-00028603.	Qy 361 PLCNQQDSIPSIQIGMFSYIVBPLFEWAHTGNSTLSENNLGHLAHNKAQWKSLLXXQ 420
XX	17-SEP-1999;		Db 361 PLCNQQDSIPSIQIGMFSYIVBPLFEWAHTGNSTLSENNLGHLAHNKAQWKSLLXXQ 420
XX	(PFIZ) PFIZER LTD.		Qy 421 HRSRGSSGGPDHDAGQGTESSEQ-EGDSP 450
XX	(PFIZ) PFIZER INC.		Db 421 HXRXGSG---QDXAGXXXXXXEQTGXP 446
PI	Fidock M;		RESULT 11
XX	DR; 2000-433274/38.		AAV93573
XX	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,		ID AAV93573 standard; protein; 445 AA.
XX	DT 25-SEP-2000 (first entry)		XX

Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

OS Synthetic.

XX Location/Qualifiers

Key Misc-difference 12 /label= Val, Ile

FT Misc-difference 16 /label= Ser, Asn

FT Misc-difference 18 /label= Glu, Asp

FT Misc-difference 20, .21 /label= Ser, Val, Asn, Ala

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 30 /label= Val, Ile

FT Misc-difference 39 /label= Pro, Arg

FT Misc-difference 56 /label= Asn, Ser

FT Misc-difference 59 /label= His, Tyr

FT Misc-difference 114 /label= Thr, Met

FT Misc-difference 141 /label= Ser, Thr

FT Misc-difference 168, .169 /label= Gly, His, Ser, Gln

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 307, .308 /label= Asp, Ala, Asn, Val

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 350 /label= Glu, Asp

FT Misc-difference 379 /label= Ser, Thr

FT Misc-difference 391 /label= His, Arg

FT Misc-difference 404 /label= Gly, Ser

FT Misc-difference 418, .419 /label= Pro, Arg, Ser, Asn

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 423 /label= Ser, Arg

FT Misc-difference 427, .428 /label= Ser, Gly, Pro, Asp, His, Gln

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 430 /label= His, Leu

FT Misc-difference 433, .434 /label= Gln, Gly, Thr, Pro, Ala

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 436, .437 /label= Ser, Glu, Thr, Leu

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

FT Misc-difference 440 /note= "optionally absent"

FT Misc-difference 443, .444 /label= Asp, Ser, Ala, Thr

FT /note= "these residues are a peptide comprising at least two or more of the above residues"

PN EP1018559-A1.

XX 12-JUL-2000.

PD 99EP-00308902.

XX 09-NOV-1999;

PF 99EP-00308902.

XX 23-DEC-1998;

PR 99GB-00028603.

XX 17-SEP-1999;

PR 99GB-00022123.

PA (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

XX Fidock M;

XX DR WPI; 2000-433274/38.

PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

XX Disclosure; Page 64-66; 104pp; English.

PS The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The present sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g., by enzyme linked immunosorbant assay (ELISA)).

XX Sequence 445 AA;

Query Match 89.9%; Score 2165.5; DB 3; Length 445;

Best Local Similarity 91.3%; Pred. No. 8,7-203; Matches 411; Conservative 1; MisMatches 33; Indels 5; Gaps 1;

QY 1 MSCIMVERGEIILFENPDQDNNAKCVMLGDPILRRLRQGTGVRAERRSYPFDERLNRISRTYS 60

Db 1 MSCIMVERGEIILFENPDQDNNAKCVMLGDPILRRLRQGTGVRAERRSYPFDERLNRISRTYS 60

QY 61 GEICTKKKVKKRLLSFQYFHASRLLRGIIQPAQLHLLDEDYLGQRHMLSKVGWMDFDIF 120

Db 61 GEICTKKKVKKRLLSFQYFHASRLLRGIIQPAQLHLLDEDYLGQRHMLSKVGWMDFDIF 120

QY 181 VTQAMHCYLIKEPKLASFLTPLDIMGLLAAAHDVDPGCVNQPFLLIKTNHHLANLYQNNS 240

Db 181 VTQAMHCYLIKEPKLASFLTPLDIMGLLAAAHDVDPGCVNQPFLLIKTNHHLANLYQNNS 240

QY 121 LFDRITNGSLVTLCHLCLPNTGHLIIRFKCDMTLHLRFLVQDFTISCPYNAVAHD 180

Db 121 LFDRITNGSLVTLCHLCLPNTGHLIIRFKCDMTLHLRFLVQDFTISCPYNAVAHD 180

QY 241 VLENHHRWSTIGMRESRLLAHLPKEMTDIEQQLSLLATDINRNEFLTRIKAHLHN 300

Db 241 VLENHHRWSTIGMRESRLLAHLPKEMTDIEQQLSLLATDINRNEFLTRIKAHLHN 300

QY 301 KDLRLEDAQRHFMQJIAALKCADINCPRIWENSKQMSERVICEFPRQCBLEQKFELTS 360

Db 301 KDLRLEXXQDRHFMQJIAALKCADINCPRIWENSKQMSERVICEFPRQCBLEQKFELTS 360

Qy	3_61	PLCNCQKDSPSIQQGFMSTIVEPLPREWAFTGNSTLSENNMLGLAHNKQOWKSLLPQ	420
Db	3_61	PLCNCQKDSPSIQQGFMSTIVEPLPREWAFTGNSTLSENNMLGLAHNKQOWKSLLXQ	420
Qy	4_21	HRSRGSSGSPDPDHAGQGTSEEEQGDSP	450
Db	4_21	HRXRGSX----XDAQXXEXEQTEGXXP	445
RESULT 1.2			
	AAV93572	Amino acid sequence of a phosphodiesterase enzyme.	
ID	AAV93572	standard; protein; 437 AA.	
XX			
AC	AAV93572;		
XX			
DT	25-SEP-2000	(first entry)	
XX			
DB		Amino acid sequence of a phosphodiesterase enzyme.	
XX			
OS		Phosphodiesterase; PDE-XIV; enzyme.	
XX			
SYNTHETIC		Synthetic.	
XX			
FH			
Key			
PT	Misc-difference 12	Location/Qualifiers	
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 16		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 18		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 20		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 29		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 38		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 55		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 58		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 113		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 140		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 167		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 305		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 347		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 376		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 388		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 401		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 415		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 419		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 423		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 425		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 428		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 430		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 433		
PT	/note= "any suitable peptide sequence or amino acid"		
PT	Misc-difference 436		
PT	/note= "any suitable peptide sequence or amino acid"		

PN	EP1018559-A1.							
XX	XX							
PD	12-JUL-2000.							
XX	PR	09-NOV-1999;	99EPB-00308902.					
PF	PR	23-DEC-1998;	98GB-00028603.					
XX	PR	17-SEP-1999;	99GB-00022123.					
PA	{PTIZ }	PFIZER LTD.						
PA	{PTIZ }	PFIZER INC.						
XX	PTI	Fidock M;						
XX	XX	DR	WPI; 2000-433274/38.					
XX	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.							
XX	Disclosure; Page 58-60; 104pp; English.							
XX	CC	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).						
XX	SQ	Sequence 437 AA;						
	Query	Match	88.1%	Score 2121;	DB 3;	Length 437;		
	Best	Local Similarity	91.9%	Pred. No. 1..9e-198;				
	Matches	411;	Conservative	1;	Mismatches	23;	Indels	12;
							Gaps	6;
Qy	1	MSCLMVERCGEILFENPDONAKCVCMLGDIRLRGOTGVRAERRGSYPFDIFRLLNSTTYS	60					
Db	1	MSCLMVERCGEIXLFXEXPQ-XXKCYCMGLDXKRLRGQTGVXAERRGSYPFDIFRLNXTTXS	59					
Qy	61	GEITGKVKYKLISFORPHASRLLRGTTIPQAFLHLDEDYLQARHMLSKVGMWDIDIF	120					
Db	60	GTGKVKYKLISFORPHASRLLRGTTIPQAFLHLDEDYLQARHMLSKVGMWDIDIF	119					
Qy	121	LFDRLTNGSNLTLCHLFNTHGLIHHFKLDMYTLHRFLYMVOQEDYHSQNPYHNAVAAD	180					
Db	120	LFDRLTNGSNLTLCHLFNTHGLIHHFKLDMYTLHRFLYMVOQEDYHSQNPYHNAVAAD	178					
Qy	161	VTOAMHCYIKEPKLKLSPFLPDIMGLLAAAHDVDPGYNQPLIKTNHLANLYQNMS	240					
Db	179	VTQAMHCYIKEPKLKLSPFLPDIMGLLAAAHDVDPGYNQPLIKTNHLANLYQNMS	238					
Qy	241	VLENHHWSTIGMIRESLILAHLPKEMTDIEQOQGSILATDINRQEFLTRLKALHLN	300					
Db	239	VLENHHWSTIGMIRESLILAHLPKEMTDIEQOQGSILATDINRQEFLTRLKALHLN	298					
Qy	301	KDLRLEDQDRHFMQLQIAALKCADICNPRIWEMSKQWSERVICEEFYRQGELQKFELEIS	360					
Db	299	KDLRLE-XQDRHFMQLQIAALKCADICNPRIWEMSKQWSERVICEEFYRQGKLEQKFELEIS	357					

Qy	361 PLCNQOKSDIPSQIQGFMSSVIVEPLPREWAHFTGNSTLSENMLGHAINKAQWKSLLPPQ	420	Db	1 MSCLMVERGEGE-LFE---PQKCYCMLGD-RURGQTGV-AERGSYPPFDFRUJNTT--S	51
Db	358 PLCNQOKSDIPSQIQGFMSSVIVEPLPREWAHFTGNSTLSENMLXHAINKAQWKSLL-XQ	416	Qy	61 GEIGTKKKEVRLISFQRPHASRLLRGITPQAHLILEDYLGQARHLSKVRWDFDF	120
Qy	421 HRSRGSSGGSPDHDAQGCTESEEQEG	447	Db	52 GEIGTKKKYKVRLLISFQRPHASRLLRGITPQAHLILEDYLGQARHLSKVG-WDFDFP	110
Db	417 HRXRGSSX-----DXA-GXEXEQXEG	435	Qy	121 LFDRLTNGSLVTLCHLFNTHGLIHHPKLDMVYDHSQNCPYHNAVHAD	180
RESULT 13					
AAV93571	AAV93571 standard; protein; 413 AA.		Db	111 LFDRLTNGSLVTLCHLFN-HGLIHHPKLDMVYDHSQNCPYHNAVHAD	167
ID			Qy	181 VTQAMHCYLKEPKLASFPTPLDILM/GHLAAAANDVDHPGVNQPLIKTNHHLANLYQNMS	240
XX			Db	168 VTQAMHCYLKEPKLASFPTPLDILM/GHLAAAANDVDHPGVNQPLIKTNHHLANLYQNMS	227
AC			Qy	241 VLENHAWSTIGMRSLAHLPKEMTDIEQOLGSLILATDINRQNEFLTLKALHN	300
XX	25-SEP-2000 (first entry)		Db	228 VLENHAWSTIGMRSLAHLPKEMTDIEQOLGSLILATDINRQNEFLTLKALHN	287
DE	Amino acid sequence of a phosphodiesterase enzyme.		Qy	301 KDLRLEDAQDRHFMQLQALKCADICNPGRWVNSKQNSRVCREFYRQELBKPELETS	360
XX			Db	288 KDRLE-QDRHFMQLQALKCADICNPGRWVNSKQNSRVCREFYRQ-LEBKPELETS	344
KW	Phosphodiesterase; PDE-XIV; enzyme.		Qy	361 PLCNQOKSDIPSQIQGFMSSVIVEPLPREWAHFTGNSTLSENMLGHAINKAQWKSLLPQ	420
XX			Db	345 PLCNQOKSDIPSQIQGFM-YIVEPLPREWA-FTGNSTLSENML-HAINKAQWKSLL-Q	399
OS	Synthetic.		Qy	421 HRSRGSSGGSPDHAGQSTESBEGQ	447
XX			Db	400 HR-RGSDA-----GEEQEG	412
RESULT 14					
			AAU08676	AAU08676 standard; protein; 391 AA.	
ID			XX	AAU08676;	
			XX		
			AC		
			XX		
			AC		
			XX		
PT	18-DEC-2001 (first entry)		DT		
XX			DB		
Human phosphodiesterase type 7B #2.			DE		
XX			DB		
Human; phosphodiesterase type 7B; cardiovascular disease; asthma; allergy; inflammatory disease; immune-related disorder; cardiovascular; antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.			KW		
XX			KW		
Homo sapiens.			KW		
XX			OS		
Key			XX		
Misc-difference	188		XX		
Location/Qualifiers			XX		
/label= Unknown			XX		
/note= "Encoded by CMC"			XX		
FT			XX		
Misc-difference	188		XX		
FT			XX		
/note= "Encoded by GAR"			XX		
FT			XX		
Misc-difference	387		XX		
/label= Unknown			XX		
/note= "Encoded by GNN"			XX		
FT			XX		
WT0200162940-A2.			XX		
XX			XX		
30-AUG-2001.			PD		
XX			XX		
20-FEB-2001; 2001WO-EP001858.			PF		
XX			PR		
21-FEB-2000; 2000EP-00103655.			XX		
(MERCK) MERCK PATENT GMBH.			PA		
XX			XX		
Kluxen F, Hentsch B;			PI		
XX			XX		
WPI; 2001-570636/64.			DR		
XX			DR		
N-PSDB; AAS13249.			XX		
Qy	1 MSCLMVERGEGBILFNPDNOKCVMLGDIRLRGQTGVRAERRGSYPPFDFRUJNTSY	60			

PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
 XX diagnosing and treating, e.g. asthma, inflammation and allergies.

PS Claim 1; Page 39-40; 40pp; English.

XX The invention relates to a novel human Phosphodiesterase type 7B
 CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
 CC acid may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
 CC example, The protein and nucleic acid may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P7B by expressing
 CC inactive proteins or to supplement the patients own production of P7B.
 CC The nucleic acids may be used to produce P7B polypeptides, by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. The nucleic acid and its complements may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acids in samples, and therefore which patients may be in
 CC need of restorative therapy. The P7B polypeptides may also be used as
 CC antigens in the production of antibodies against P7B and in assays to
 CC identify modulators of it's expression and activity. The anti-P7B
 CC antibodies and antagonists may also be used to down regulate expression
 CC and activity. The anti-P7B antibodies may also be used as diagnostic
 CC agents for detecting the presence of P7B in samples (e.g., by enzyme
 CC linked immunosorbent assay (ELISA)). Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include, for example
 CC cardiovascular disease, asthma, allergy, inflammation, and immune-related
 CC disorders. The present sequence represents a human phosphodiesterase 7B
 XX sequence 391 AA;

Sequence 391 AA;

Query Match 77.5%; Score 1865; DB 4; Length 391;
 Best Local Similarity 92.7%; Pred. No. 2e-173;

Matches 354; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

Qy 52 RLLNNTTYGEIGTKKVKRLLSQRFLRGLTIPQAPLHLDDEYLGOARHMLSK 111

Db 10 RLLNNTTYGEIGTKKVKRLLSQRFLRGLTIPQAPLHLDDEYLGOARHMLSK 69

Qy 112 VGMWDFDPLFLFDRLTNGSLVTLCHLPLTHGLJHHFKLDMYTLHRFLVMDYDHQNPK 171

Db 70 VGMWDFDPLFLFDRLTNGSLVTLCHLPLTHGLJHHFKLDMYTLHRFLVMDYDHQNPK 129

Qy 172 YHNAVHAADVTQAMHCYIKEPKLASFLTPLDIMGLLAAAKDVPDHGCVNQPLIKTNHH 231

Db 130 YHNAVHAADVTQAMHCYIKEPKLASFLTPLDIMGLLAAAKDVPDHGCVNQPLIKTNHH 189

Qy 232 LANLYQNNSVLENHWRSITGMURESLRLLAHLPKEMTDIEQQLGSLTILATDINRNQFEL 291

Db 190 LANLYQNNSVLENHWRSITGMURESLRLLAHLPKEMTDIEQQLGSLTILATDINRNQFEL 249

Qy 232 TRUKAHLLANKDKDLRLEDQPRHFMQLIKEPKLASFLTPLDIMGLLAAAKDVPDHGCVNQPLIKTNHH 351

Db 250 TRUKAHLLANKDKDLRLEDQPRHFMQLIKEPKLASFLTPLDIMGLLAAAKDVPDHGCVNQPLIKTNHH 309

Qy 352 EQKPELEISPLCNQKQKOSITPSIQTIGEMSYIVPELRFWAHFCNNTSLSENMIGHLAHNKA 411

Db 310 EQKPELEISPLCNQKQKOSITPSIQTIGEMSYIVPELRFWAHFCNNTSLQRTCHWATPAHNG 369

Qy 412 QWKSLLPQRHRSRGSSGSSGPDH 433

Db 370 QWKSLLPSSTEAGAALAXLDH 391

RESULT 15

ADY50214 Standard; protein; 335 AA.

ID ADY50214;

XX DT 19-MAY-2005 (First entry)

XX Human PDE7B phosphodiesterase domain SEQ ID NO:23.

XX phosphodiesterase 7B; PDE5A; X-ray crystallography; enzyme.
 XX
 PS OS Homo sapiens.
 XX
 CC PN US2005048573-A1.
 CC PD 03-MAR-2005.
 CC PF 03-FEB-2004; 2004US-00771833.
 CC PR 03-FEB-2003; 2003US-0444734P.
 CC PR 07-JUL-2003; 2003US-0485627P.
 CC PA (PLEX-) PLEXXICON INC.
 CC PA Artis DR, Bollag G, Card G, Martin F, Milburn MV, Zhang K;
 CC PI DR WPI; 2005-202088/21.
 CC Development of ligands binding to phosphodiesterase-5A (PDE5A) comprises
 PT identifying PDE5A binding compounds, determining orientation of molecular
 PT scaffolds, identifying chemical structures of molecular scaffolds and
 PT synthesizing ligand.
 CC Disclosure; SEQ ID NO 23; 111PP; English.
 CC
 XX the invention relates to a novel method for development of ligands
 CC binding to phosphodiesterase-5A (PDE5A). The method comprises identifying
 CC one or more compounds as molecular scaffolds that bind to a binding site
 CC of PDE5A, determining the orientation of at least one molecular scaffold
 CC in co-crystals with PDE5A, identifying chemical structures of the
 CC molecular scaffolds, and synthesizing a ligand with altered binding
 CC affinity and/or binding specificity. The method to identify the potential
 CC PDE5A binding compounds comprises either removing a computer
 CC representation of a compound complexed with PDE5A or modifying a computer
 CC representation of a compound complexed with PDE5A by the deletion and/or
 CC addition of one or more chemical groups; fitting a computer
 CC representation of a compound from a computer database with a computer
 CC representation of the active site of PDE5A; and identifying compounds
 CC derived from the molecular scaffold that best fit the active site based
 CC on favorable geometric fit and energetically favorable complementary
 CC interactions as potential binding compounds; and further comprises
 CC searching a database for compounds having structural similarity to the
 CC molecular scaffold or derivative compound using a compound searching
 CC computer program or replacing portions of the compound with similar
 CC chemical structures using a compound construction computer program. The
 CC compound complexed with PDE5A is non-hydrolyzable cyclic guanosine
 CC monophosphate (cGMP) analog. The fitting comprises determining whether
 CC the compounds will interact with one or more of conserved PDE5A active
 CC site residues. The attachment component is a linker (a traceless linker)
 CC for attachment to a solid phase medium and comprises a label comprising a
 CC fluorophore. The attachment method further comprises attaching the
 CC compound or derivative to a solid phase medium through a linker attached
 CC at the energetically allowed site. The phosphodiesterase comprises
 CC conserved residues matching at least one conserved PDE5A
 CC residues. The phosphodiesterase binding compound or derivative is
 CC synthesized on the linker attached to the solid phase medium. The
 CC plurality of the compounds or derivatives is synthesized in combinatorial
 CC synthesis. The attachment of the compounds to the solid phase medium
 CC provides an affinity medium. The present sequence represents the
 CC phosphodiesterase domain of human phosphodiesterase 7B.
 XX Sequence 335 AA;
 SQ Query Match 74.8%; Score 1801; DB 9; Length 335;
 SQ Best Local Similarity 100.0%; Pred. No. 2.9e-167;
 SQ Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ 87 GIIPQAPLHLDIDYLGQARHMLSKVGMWDIFLFDRLTNGSLVTLCLHFNTNLGLIH 146
 Db 1 GIIPQAPLHLDIDYLGQARHMLSKVGMWDIFLFDRLTNGSLVTLCLHFNTNLGLIH 60

Qy	147	HFKLDMVTIHRFLYVWQEDYHSQNPYHNAVAADYTOAHNCYLKEPKLASFLTPLDIMG	206
Db	61	HFKLDMVTIHRFLYVWQEDYHSQNPYHNAVAADYTOAHNCYLKEPKLASFLTPLDIMG	120
Qy	207	LLAAAHHDYDHPGYNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMURBSRLLAHLPE	266
Db	121	LLAAAHHDYDHPGYNQPFLLKTNHHLANLYQNMSVLENHWRSTIGMURBSRLLAHLPE	180
Qy	267	MTQDIEQQSLILATDINRONEFLTRLAHLANKDLRLEDADRHEMLQALKCADICN	326
Db	181	MTQDIEQQSLILATDINRONEFLTRLAHLANKDLRLEDADRHEMLQALKCADICN	240
Qy	327	PCR1WBMSK9SERVICEFYRGELBKPFLEISPLCNOQKDSIPTSIQIGFMSYIVVEPLP	386
Db	241	PCR1WBMSK9SERVICEFYRGELBKPFLEISPLCNOQKDSIPTSIQIGFMSYIVVEPLP	300
Qy	387	REWAHTGNSTLSENMLGHLAHNKAQWKSSLPROH	421
Db	301	REWAHTGNSTLSENMLGHLAHNKAQWKSSLPROH	335

Search completed: March 10, 2006, 19:56:52
 Job time : 167.463 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	Gencore version 5.1.7	3',5'-cyclic-nucle
OM protein - protein search, using bw model		3',5'-cyclic-GMP P
Run on:	March 10, 2006, 19:57:15 ; Search time 31.0976 Seconds	3',5'-cyclic GMP P
	(without alignments) 1392.313 Million cell updates/sec	cyclic nucleotide
Title:	US-10-781-181-5	cyclic nucleotide
Perfect score:	2408	cAMP-inhibited cAMP
Sequence:	1 MSCLMVERGBEILPENPDQN.....PDHDHAGGCTESBEGQGDSP 450	3',5'-cyclic-GMP P
Scoring table:	BLOSUM62	3',5'-cyclic-GMP P
	Gapop 10.0 , Gapext 0.5	3',5'-cyclic-GMP P

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	100.0	450	2 JC7266	3',5'-cyclic-nucle
2	1419.5	58.9	498	2 A47286	3',5'-cyclic-nucle
3	604.5	25.1	673	2 I61358	3',5'-cyclic-nucle
4	603.5	25.1	584	2 B53109	3',5'-cyclic-nucle
5	603.5	25.1	672	2 I61259	CAMP phosphodiesterase
6	580.5	24.1	562	2 I59143	cyclic AMP phospho
7	580.5	24.1	564	2 A40949	3',5'-cyclic-nucle
8	567.5	23.6	564	2 JC1519	phosphodiesterase
9	567.5	23.6	736	2 I61354	3',5'-cyclic-nucle
10	555.5	23.5	886	2 A54442	3',5'-cyclic-nucle
11	555.5	23.2	610	2 I67946	phosphodiesterase
12	559.5	23.2	844	2 I52865	3',5'-cyclic-nucle
13	553	23.0	712	2 S71626	3',5'-cyclic-nucle
14	529.5	22.0	536	2 T16745	hypothetical prote
15	517	21.5	549	2 T16769	3',5'-cyclic-nucle
16	493	20.5	777	2 S65543	CAMP phosphodiesterase
17	477.5	19.8	323	2 S55348	3',5'-cyclic-nucle
18	468	19.4	267	2 B33904	hypothetical prote
19	468	19.4	535	1 A46378	3',5'-cyclic-nucle
20	466	19.4	534	1 A44162	3',5'-cyclic-nucle
21	466	19.4	519	2 T14783	hypothetical prote
22	466	19.4	535	1 A44161	3',5'-cyclic-nucle
23	461	19.1	664	2 T24459	hypothetical prote
24	454.5	18.9	530	1 A45334	3',5'-cyclic-nucle
25	452.5	18.8	788	2 T10196	3',5'-cyclic-nucle
26	449	18.6	536	1 JC6129	3',5'-cyclic-nucle
27	445.5	18.5	713	2 JWD088	3',5'-cyclic-nucle
28	441	18.3	659	2 JBD93	3',5'-cyclic-nucle
29	441	18.3	885	2 JC7989	3',5'-cyclic nucle

ALIGNMENTS

RESULT 1	JC7266	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human
N;Alternate names:	CAMP-specific phosphodiesterase 7B	C;Species: Homo sapiens (man)
C;Date:	18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004	C;Accession: JC7266
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.	Biochem. Biophys. Res. Commun. 271, 575-583, 2000	A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.
A;Reference number: JC7266	A;Molecule type: mRNA	A;Accession: JC7266
A;Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040	A;Map position: 6q23-24	C;Keywords: phosphoric diester hydrolase
A;Experimental source: caudate nucleus	C;Genetics:	
A;Gene: pde7B		
A;Map position: 6q23-24		
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-cyclic-nucleotide phosphodiesterase 1B, human		
A;Cross-references:		
A;Experimental source:		
C;General:		
Query Match	100.0%	Score 2408
Best Local Similarity	100.0%	Pred. No. 5.4e-182;
Matches 450;	Conservative 0;	Indels 0;
	Missmatches 0;	Gaps 0;
Qy 1 MSCLMMVERCGELLFENPDQNAKCVCMGLDIRERGOTGVAERRGSYPRIDERLINSRTYS 60		
Db 1 MSCLMMVERCGELLFENPDQNAKCVCMGLDIRERGOTGVAERRGSYPRIDERLINSRTYS 60		
Qy 61 GEITGTRKKVRLRLLFSQRYFHASRLLRGITIPQAPLHLIDEDYUQARAHMLSKVGMWDFP 120		
Db 61 GEITGTRKKVRLRLLFSQRYFHASRLLRGITIPQAPLHLIDEDYUQARAHMLSKVGMWDFP 120		
Qy 61 LPDRLTNGNSLVTLCHLFNTNGLIHFNLKDTYFLRPLMVQDVSQNPYHNAVRAD 180		
Db 121 LPDRLTNGNSLVTLCHLFNTNGLIHFNLKDTYFLRPLMVQDVSQNPYHNAVRAD 180		
Qy 181 VTOQAMHCYLKEPKLASEPTLDIMLGLLAAAHVDHPGVNQPLFLKTNNHLANLYQNM 240		
Db 181 VTQAMHCYLKEPKLASEPTLDIMLGLLAAAHVDHPGVNQPLFLKTNNHLANLYQNM 240		
Qy 241 VLENHHRSTIGMLRSLRLLAHPKMTDIEQLQSSLLATDINRQNEFLTRKLHN 300		
Db 241 VLENHHRSTIGMLRSLRLLAHPKMTDIEQLQSSLLATDINRQNEFLTRKLHN 300		
Qy 301 KDLRLIEDAQDRHFMLOIAALKCADICNCPRIWMSKOWSERVEEFYRQGELEQKFELIS 360		
Db 301 KDLRLIEDAQDRHFMLOIAALKCADICNCPRIWMSKOWSERVEEFYRQGELEQKFELIS 360		
Qy 361 PLCNQKDSDIPSQIQGEMSYIPEPLFREWAHTGNSTSENMLGHANAKQWSLPRQ 420		

Db	361	PLCNQQKOSIPSQIQGMNSYIVEPLFREWAHFTGNSTLSENMLGHIAHKNAQWKSLLPRQ	420	A; Reference number: A54442 ; MUID: 94019330 ; PMID: 8413254 A; Accession: I61358 A; Status: translated from GB/EMBL/DBJ A; Molecule type: mRNA A; Residues: 1-673 <RES> A; Cross-references: UNIPARC:UPI0000050EB5 ; GB:L20970; NID:g347129; PIDN:AAA03592_1; PID:5 R; Baeker, P.A.; Obernolce, R.; Bach, C.; Yee, C.; Shelton, E.R. Gene 138, 253-256, 1994
Qy	421	HSRGSSGGPDDHAGGCTTESREOEGDSP	450	A; Reference number: I38416 ; MUID: 9433346 ; PID: 002882 ; NID: 9433346 ; PMID: 8125310
Db	421	HSRGSSGGPDDHAGGCTTESREOEGDSP	450	C; Species: Homo sapiens (man) C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000 C; Accession: A47286 R; Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers J.; Bio. Chem. 268, 12925-12932, 1993 A; Title: Isolation and characterization of a previously undetected human cAMP phosphodiesterase 3,5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment) A; Cross-references: UNIPARC:UPI0001440B6 ; GB:L12032; NID:g179892; PID:9179893 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent ; 3',5' C; Keywords: phosphoric diester phosphodiesterase homology <CNP> F;227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Qy	7	ERCGEILFENPDQNAKCVCMGLDIRLGQTGVRAERRGSYPIDERLNNSTYSGEIGTK	66	Score 58.9†; Best Local Similarity 61.7†; Pred. No. 56-104; Mismatches 70; Indels 1; Gaps 1; Matches 261; Conservative 135; Score 141.9.5†; DB 2; Length 498;
Db	62	QFRGAISSDSDSSTTDTALTYTRMLGQVRSRAGFESERGSHPYTDIFRHFQSEIEVSYVS	121	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 66 KKVKVRLLS---FORYEHASRLLRQGIPQAPLHLDEDYLGOARHMLSKVGMWDDDFIPL 121 218 KBKKKRPMSQISGVKLHMSSLTNSSPREGVKTQEVDLAKE--LEDVNWKGGHVFR 274
Qy	7	KKVRLLSPQRYFHASRLLRQGIPQAPLHLLDQDYLQARAHLSKGWMDPDIFLDRLT	126	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 122 FDRLLTNGNSLYTLCH-LFNTFHGLIHFKLDMVTHRFELMVMQEDYHSQNPNYHNAAD 180 275 IAEL-SGNRPITVTTQFQERDLKMTKEPVDTLTLTYLMTLDEHYADYAHNNHAAD 333
Db	122	RNTRLLSFQYLRSSRFFRTAVSNSLNLDYYCQAQKCMLEKVGWNWDFIFLDRLT	181	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 181 VTOAMCYCLKEPKLAFSLTPDIDMUGLALAHDVHPGIVNQPFLLKTNHHLANLYQNMS 240 334 VVQSTVNLSTPALEVFTDLELAIAFSAIHDVHPGSNQFLINTNSELALMYNDSS 393
Qy	127	NGNSLVTLTLCFLFNTHGLIHHFKLDMVTHRFELMVOEDYHSQNPNYHNAADYTOAHE	186	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 241 VLENTHWRSTIGMLRCSR--LLAHLPKEMTQDIEEOGLSLLATDINRNEFLTRIKAHL 298 394 VLENHHLAVGPFLQDENCFQNLTRKQFOSLKRKVIDIVLATDHSKMNLLADIKTMV 453
Db	182	NGNSLVSLTFLHFSLHLIELYFLDMKMLRRLPFLQEDYHSQNPNYHNAADYTOAHE	241	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 299 HNKD----LRLEDAQDRHFMQLQALKCADICNPGRIMWSKQMSBRVCBEFYRQGELE 352 454 ETKVVTSQVLLNHRCAQDLSQVQLNWVHACDLSNPQKPLQYRQDTRDMEBFFRGDRE 513
Qy	187	CYLTKEPKLAFSLTPLDIMALGLIAAAHDVDPFGVNOFPFLIKTNHHLANLYQNMSVLENHH	246	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 353 QKFELEISPLCNCQKDSIPSITQIGMNSYIVEPLFREWAHFTGNSTLSENMLGHIAHKNAQ 412 514 ERGMESISPMDKHNAAVSERSQVGFIDYVHPLWETADLVHPD--AQDIDLTLDENRNEW 571
Db	242	CYLTKEPKLAFSLTPLDIMALGLIAAAHDVDPFGVNOFPFLIKTNHHLANLYQNMSVLENHH	301	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 413 WKSLLPQRHRSRGSSSGPDDHACQGTSE-----EQEGDS 449 572 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Qy	247	WRSTIGMLRESRLAHLPKEMTQDIEOGLSLLATDINRNEFLTRIKAHLHKNKDLRL	306	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 573 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Db	302	WRSAVGILRESGFSLHPLPESRQQMTOQIGAILATDISRQEYLSLFRSHLDRGDLCL	361	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 574 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Qy	307	DAQDRHFMQLQALKCADICNPGRIMWSKQMSBRVCBEFYRQGELE	366	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 575 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Db	362	DTRHRHLVLQWMLAKPKCADICNPGRIMWSKQMSBRVCBEFYRQGELE	421	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 576 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Qy	367	KDSIPISTQIGMNSYIVEPLFREWAHFTGNSTLSENMLGHIAHKNAQWKSLLPRQSRGS	426	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 577 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Db	422	TESIANQIGMNTLYVEPLFTWAEARS-NTRISQTMGLHGVLANKASWKGQREQSSSED	480	Query Match 5.1%; Best Local Similarity 33.3%; Pred. No. 1..3e-39; Matches 86; Mismatches 151; Indels 33; Gaps 9; Query 578 YQSTRIPQ-----SPSPAPDDPEEGRQGQTEKFQFBETLBEDGES 610
Qy	427	SGS 429	427 SGS 429	RESULT 4 B53109 3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, rolipram-sensitive C; Species: Rattus norvegicus (Norway rat) C; Accession: B53109; A34414; C33904; 167944
Db	481	DAA 483	Db 481 DAA 483	A; Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP pi A; Reference number: A53109 ; MUID: 94103234 ; PMID: 8276818 A; Accession: B53109 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-584 <MON> A; Cross-references: UNIPROT:P14270; UNIPARC:UPI00002A6E1; GB:U01280
RESULt 3	161358	3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human	RESULt 3 161358 C; Species: Homo sapiens (man) C; Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000 R; Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 658-6571, 1993 A; Title: A family of human phosphodiesterases homologous to the dunce learning and memory	A; Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormone

A; Reference number: A34414; MUID: 90046763; PMID: 2554303

A; Accession: A34414

A; Molecule type: mRNA

A; Residues: 1-584 <SWI>

A; Cross-references: UNIPARC:UPI000002A6E1; GB:U09455; GB:M25349; NID:9517501; PIDN:AAA20

R; Swinnen, J.V.; Joseph, D.R.; Conti, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 5225-5229, 1989

A; Title: Molecular cloning of rat homologues of the Drosophila melanogaster duncane cAMP F

A; Reference number: A33904; MUID: 89315790; PMID: 2546153

A; Accession: C33904

A; Molecule type: mRNA

A; Residues: 214-480 <SWI>

A; Cross-references: UNIPARC:UPI00001759B1; GB:M25349

A; Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes

A; Reference number: I53865; MUID: 95047482; PMID: 7958996

A; Accession: 167944

A; Molecule type: mRNA

A; Residues: 'EFPEBS', '34-421', 'E', '423-584' <RES>

A; Cross-references: UNIPARC:UPI00001759B2; GB:L27060; NID:9436009; PID:9436010

C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'

C; Keywords: alternative initiators; alternative splicing; cAMP binding; phosphoric diest

F; P=37-465/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 25.1%; Score 603.5; DB 2; Length 584;

Best Local Similarity 33.3%; Pred. No. 1.5e-39; Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

Query 66 KKKVKRKL-----FQYRFHASRLRGITPOAPLHLLDBDYLQAREHMLSKVGMWDFDIFL 121

Db 130 KERKGRMNSQISGVCKLMHSSSLTNSCIPRFVKTEQDVLAKE---LEDYNRWGHLHVR 186

Qy 122 FDLTLNGNSLVTLCH-LFNTGHLHFKLDMVTLHFLVWQEDYHSQNQPHNATHAD 180

Db 187 TAL-SGNRPLTVIMHTFQERDLKLTFKIPDFTLTYLLEDHYHADYHNNTHAAD 245

Qy 181 VTOAMHCYLKEPKLASLTPLDIMLGILAAAHDDHPGVNQPLKTKNPHILANLYQHMS 240

Db 246 VVQSTHVLLSTPALEAVFTDLELIAAFASAHHDVDPGSNQFLINTNSEALMYNDSS 305

Qy 241 VLENHHWRSTIGMLRESR--LIAHLHPKEMTQDEQOLQSLTILATDINRQNBFTRLK AHL 298

Db 306 VLENHHHLAVGFKLQBNCDIFONLTQKQRQSRKMDIVIATDKHNMILLADIKTMV 365

Qy 299 HNKD-----LRLEDAQRHFMQLQALKCADICNPCKIWEKSERVCEPYRQGEL 352

Db 366 ETKKVTTSSGGVLLDNYSRDIQVLMNVHCADLSNPTPKLQYRWTDRIMEEFFRCQDRE 425

Qy 353 QPKELLESPLCNQKQSIKPSIQTQGMSYIVEPFLPRAHFHTGNSTSSENMLGHLAHKAQ 412

Db 426 RERGMESPMCDKGNAVSQFQGFDIYVHPLWETADLVHPD-AQDILDTLEDNREW 483

Qy 413 WKSLLPROHRSRGSSGGSGPDDHAGQCTSE-----EGQGDS 449

Db 484 YQSTRIPQ-----SPSPAPDDQBDGQGQTEKFQFFLTLEDGES 522

RESULT 6

159143

CAMP Phosphodiesterase - rat (fragment)

C; Species: Rattus norvegicus (Norway rat)

C; Date: 02-Jul-1996 #text_change 09-Jul-2004

C; Accession: 159143

R; Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989

A; Title: Isolation and characterization of a mammalian gene encoding a high-affinity CAMI

A; Reference number: 159143; MUID: 892644; PMID: 2542941

A; Accession: 159143

A; Status: Preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-562 <RES>

A; Cross-references: UNIPROT:P14646; UNIPARC:UPI00001440B1; GB:J04563; NID:9203967; PMID: 1

C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'.

J. Biol. Chem. 269, 18271-18274, 1994

A; Title: The rat DDE3/IVD phosphodiesterase gene codes for multiple proteins differential

A; Reference number: A53678; MUID: 9430845; PMID: 8034568

A; Accession: 161259

F:231-459/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 562;

Best Local Similarity 31.9%; Prod. No. 7.7e-38; Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

Qy 66 KKKVKRILS---FORYFASRLRGITPPQPHLLEDYLGARHMLSKVGMWDFDIEL 121
Db 124 KCKKQQLMTOISGVKKLMHSSSLNNTTSRFGNTENEDHLAKELDILNK---WGANIEN 180Qy 122 FDLTNGNSLVTLLCHLPNTGHLJHKFLDMYTLHRFLVMYQDDEYSQNPTENAVHAADV 181
Db 181 VAGYSHNRPLTCIMYAFQERDLKTFKISSDTFTVYMMTLEDHYRSDVATHNSLHAADV 240Qy 182 TOAMHCYLIKPEKLASFLLPDLIMGLIAAAAHDVDPHCNVNQPLIKTNHHLANLYQMSV 241
Db 241 AOSTHVLLSTPAIDAVFTDLEIAIAFAAITHDVDHGVSNOFLINTNSEALMYNDENV 300Qy 242 LENHHWRSTIGMRESR---LLAHLPKEMTDIEQQLGLSLILATDINRQNELLTRIKAHLL 299
Db 301 LENHHLAVGFKLQEEBCDIFQNLTKCORQTRKMTDMVLTADMSCHMSLLADLKTMVE 360Qy 300 NWD-----LRLEDAQDPHFMQIAALKACDNCPTRIWMSKQWSERVICEEFYRQEGLQ 353
Db 361 TRKVTTSGVLLDNTRIOVLRNMYCADLSNPTSSLERYQWTDRIMBEFFEQQSDKER 420Qy 354 KFELEISPLCNQODSIPSIQIGFMSYITPEPLFREWAHTGNSTLSNMLGHLAINKAOW 413
Db 421 ERGMEISPMCDRHTASVEKSQVGFIDYIVHPMETWDLVQPD--ADIDLTLDEDRNWTY 478Qy 414 KSLLPR----QHRSNGSSGSGPDDH---AGOGTESESEQEGDSP 450
Db 479 QSMIPQSPPSPPLDERSDCQGIMBKQFQELTUEBDEPEKEEGP 525

RESULT 7

CYCLIC-AMP phosphodiesterase (EC 3.1.4.-) - rat

C:Species: Rattus norvegicus (Norway rat)
C:Accession: A40949; D33904; A53109; I167942
R:Svinnen, J.V.; Tsikalis, K.E.; Conti, M.J. Biol. Chem. 266, 18370-18377, 1991.
A;Title: Properties and hormonal regulation of two structurally related cAMP phosphodiesA;Reference number: A40949; MUID: 92011575; PMID: 1655746
A;Status: preliminaryA;Molecule type: mRNA
A;Cross-references: UNIPARC:UP100001759B3; GB:M25350A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster duncane cAMP P
A;Reference number: A33904; MUID: 89315790; PMID: 2546153
A;Status: preliminaryA;Molecule type: mRNA
A;Cross-references: UNIPARC:UP1000014C5AB; GB:M97515; NID:9292387; PID: AAA36426.1; PID: 5A;Sequence extracted from NCBI backbone (NCBIN: 127928, NCBIPI: 127930)
J. Biol. Chem. 268, 6470-6476, 1993
R:Boiger, G.B.; Michaelis, T.; Martins, T.; Steiner, B.; Rodgers, L.; Riggs, N.Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the duncane learning and memory genesA;Reference number: A54442; MUID: 94019330; PMID: 94019330
A;Reference number: A54442; MUID: 8413254A;Accession: 167942
A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-564 <RES>

A;Cross-references: UNIPARC:UP100002A69; GB:L27058; PID:950096; calmodulin-dependent 3', 5'-

C;Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B

C;Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase

F:233-461/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 564;

Best Local Similarity 31.9%; Pred. No. 7.7e-38; Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

Qy 66 KKKVKRILS---FORYFASRLRGITPPQPHLLEDYLGARHMLSKVGMWDFDIEL 121
Db 124 KCKKQQLMTOISGVKKLMHSSSLNNTTSRFGNTENEDHLAKELDILNK---WGANIEN 180Qy 122 FDLTNGNSLVTLLCHLPNTGHLJHKFLDMYTLHRFLVMYQDDEYSQNPTENAVHAADV 181
Db 181 VAGYSHNRPLTCIMYAFQERDLKTFKISSDTFTVYMMTLEDHYRSDVATHNSLHAADV 240Qy 182 TOAMHCYLIKPEKLASFLLPDLIMGLIAAAAHDVDPHCNVNQPLIKTNHHLANLYQMSV 241
Db 241 AOSTHVLLSTPAIDAVFTDLEIAIAFAAITHDVDHGVSNOFLINTNSEALMYNDENV 300Qy 242 LENHHWRSTIGMRESR---LLAHLPKEMTDIEQQLGLSLILATDINRQNELLTRIKAHLL 299
Db 301 LENHHLAVGFKLQEEBCDIFQNLTKCORQTRKMTDMVLTADMSCHMSLLADLKTMVE 360Qy 300 NWD-----LRLEDAQDPHFMQIAALKACDNCPTRIWMSKQWSERVICEEFYRQEGLQ 353
Db 361 TRKVTTSGVLLDNTRIOVLRNMYCADLSNPTSSLERYQWTDRIMBEFFEQQSDKER 420Qy 354 KFELEISPLCNQODSIPSIQIGFMSYITPEPLFREWAHTGNSTLSNMLGHLAINKAOW 413
Db 421 ERGMEISPMCDRHTASVEKSQVGFIDYIVHPMETWDLVQPD--ADIDLTLDEDRNWTY 478Qy 414 KSLLPR----QHRSNGSSGSGPDDH---AGOGTESESEQEGDSP 450
Db 479 QSMIPQSPPSPPLDERSDCQGIMBKQFQELTUEBDEPEKEEGP 525

RESULT 8

C:Species: Homo sapiens (man)
C:Accession: JCI1519; A45500; I61359

R:Obenreuter, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Multkins, M.; Jarnagin, K.

Gene 129, 239-247, 1993
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a nA;Reference number: JCI1519; MUID: 93314568; PMID: 8392015
A;Molecule type: mRNA
A;Accession: JCI1519

A;Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014C5AB; GB:L12688

A;Sequence given
A;Experimental source: lymphocyte

A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:9292387; PID: AAA36426.1; PID: 5

A;Sequence extracted from NCBI backbone (NCBIN: 127928, NCBIPI: 127930)
R:McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.J. Biol. Chem. 268, 6470-6476, 1993
A;Title: A low Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.f mRNA.
A;Reference number: A45500
A;Accession: A45500A;Molecule type: mRNA
A;Residues: 1-564 <RES>

A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:9292387; PID: AAA36426.1; PID: 5

A;Sequence given
A;Experimental source: frontal cortex

A;Cross-references: UNIPARC:UPI00001759B3; GB:M25350

A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster duncane cAMP P

A;Reference number: A33904; MUID: 89315790; PMID: 2546153
A;Status: preliminaryA;Molecule type: DNA
A;Residues: 210-476 <SW2>

A;Cross-references: UNIPARC:UP100001759B3; GB:U01291; PID:9409826; PID:AAA18926.1; PID:

A;Reference number: 153865; MUID: 95047482; PMID: 7958996

A;Accession: 161359	A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ	Db	415	AQSTVLLSTPALDAVFTDELLAIAPIAAAHVDHPGSNQFLINTNSEALMNYDESV 474
A;Molecule type: mRNA		Qy	242	LENHWRSTGMLRESR--LLAHIPKEMTDIEQQLSLLATDINRQEFLTRKAKHL 299
A;Residues: 1-564 <RES>		Db	475	LENHHLAVCFKLLOEEHCDPFLNITKQQTILRQMSKMSLLADLTMVE 534
A;Cross-references: UNIPARC:UPI000014C5AB; PIDN:AAA03593_1; PID: F;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'		Qy	300	NKD----IRLEDAQRDHFMQLTALKACDADCNPCRWNSKWSERVICEFYRGQEQ 353
C;Keywords: phosphoric diester hydrolase		Db	535	TCKVTSGVLLDNTYDRQVLRAVNHCADLSNPTKSLEYRWTDLMEFFQQDKE 594
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>		Qy	354	KPELFISPLCNQKQDSIPTSIQGMSTYVPLFREWAHTFGNSTLSENNLGHIAHNKAQW 413
Query Match Score 567.5; DB 2; Length 564;		Db	595	ERGEISIPNCDCIKTASVKSQVGFIDYVHPLWETADLYQPD-AQDILDTLEDRNWY 652
Best Local Similarity 31.3%; Pred. No. 8.1e-37; Mismatches 149; Indels 41; Gaps 8;		Qy	414	KSLLPQRHRSRGSSGGP---DHDHAG-----QGTSESBQEGD 418
Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;		Db	653	QSMIQP-----SPSPPLDEQRNDQGLMEKEQFELTLDEBEDSEGPEKEGE 637
Qy		Db		
66 KKKVKRLLS---FORYPHASRLRGTIPQAPLHLLDDYLGQARHMLSKVGWMDFDIFL 121		Qy		
126 KKKQQLMTQISCVKLMHSSSLNTTSRFGNTENDHAKLEBLINK--WGLNLFN 182		Db		
122 FDLTGNSLVTLCLHFNTLGHFLKLDMTLHRFLVMQDHYHSQNPYHNVAHAADV 181		Qy		
183 VAGYSNRPRLTCIMYALFQERDLKTFNISDIFTYNTMFLEDHYSDVAYNLSHAADV 242		Db		
182 TOAMHCYLKPKLASFLTPLDINGLIAAAAHVDHPGVNQPLPLIKNHHLANLYQNMIV 241		Qy		
243 AOSTHVLLSTPALDAVFTDELLAIAPIAAAHVDHPGVNQPLPLIKNHHLANLYQNMIV 302		Db		
242 LENHWRSTGMLRESR--LLAHIPKEMTDIEQQLSLLATDINRQEFLTRKAKHL 299		Qy		
303 LENHHLAVCFKLLOEEHCDPFLNITKQQTILRQMSKMSLLADLTMVE 362		Db		
300 NKD----IRLEDAQRDHFMQLTALKACDADCNPCRWNSKWSERVICEFYRGQEQ 353		Qy		
363 TCKVTSGVLLDNTYDRQVLRAVNHCADLSNPTKSLEYRWTDLMEFFQQDKE 422		Db		
354 KPELFISPLCNQKQDSIPTSIQGMSTYVPLFREWAHTFGNSTLSENNLGHIAHNKAQW 413		Qy		
423 ERGMEISIPMCDDHTASVKSQVFDIYVHPLWETADLYQPD-AQDILDTLEDRNWY 480		Db		
414 KSLLPQRHRSRGSSGGP---DHDHAG-----QGTSESBQEGD 448		Qy		
481 QSMIQP-----SPSPPLDEQRNDQGLMEKEQFELTLDEBEDSEGPEKEGE 525		Db		
RESULT 9		Qy		
161359	A;Cross-references: UNIPROT: P27815; UNIPARC:UPI0000047003; PID: 934711; PID: 918087; NID: 600126	Db		
C;Species: Homo sapiens (man)		Qy		
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004		Db		
C;Accession: 161354		Qy		
R;Boger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993		Db		
A;Title: A family of human phosphodiesterases homologous to the duncle learning & memory protein kinase. A;Reference number: A5442; PMID: 94019330; PMID: 8413254		Qy		
A;Status: translated from GB/EMBL/DDJB		Db		
A;Molecule type: mRNA		Qy		
A;Residues: 1-886 <RES>		Db		
A;Cross references: UNIPROT: P27815; UNIPARC:UPI0000047003; PID: 934711; PID: 918087; NID: 600126		Qy		
A;Note: 736-Ala was also found		Db		
R;Livi, G.P.; Kmatz, P.; McNamee, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.		Qy		
Mol. Cell. Biol. 10, 2678-2886, 1990		Db		
A;Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive A;Reference number: A36317; PMID: 2160582		Qy		
A;Status: preliminary		Db		
A;Molecule type: mRNA		Qy		
A;Residues: 'MCPPFPVTV',210-735,'E','737-886 <SUL>		Db		
A;Cross references: UNIPARC:UPI00000246C; EMBL:U18087; NID: 9604374; PIDN: AAC5050		Qy		
A;Gene: PDE4A; DPDE2		Db		
A;Cross references: GDB: 138776; OMIM: 600126		Qy		
A;Map position: 1p31.3-1q912		Db		
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase F;432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>		Qy		
Query Match Score 565; DB 2; Length 886;		Db		
Best Local Similarity 32.1%; Pred. No. 2.4e-36; Mismatches 165; Indels 20; Gaps 6;		Qy		
Matches 126; Conservative 82; Mismatches 165;		Db		
Qy		Qy		
66 KKKVKRLLS---FORYPHASRLRGTIPQAPLHLLDDYLGQARHMLSKVGWMDFDIFL 121		Db		
298 KKKQQLMTQISCVKLMHSSSLNTTSRFGNTENDHAKLEBLINK--WGLNLFN 354		Qy		
122 FDLTGNSLVTLCLHFNTLGHFLKLDMTLHRFLVMQDHYHSQNPYHNVAHAADV 181		Db		
355 VAGYSNRPRLTCIMYALFQERDLKTFNISDIFTYNTMFLEDHYSDVAYNLSHAADV 414		Qy		
182 TOAMHCYLKPKLASFLTPLDINGLIAAAAHVDHPGVNQPLPLIKNHHLANLYQNMIV 241		Db		

Qy	189	LKEPLASFTPTLDLMLGLAAADVDHPGVNQPLIKTNHHLANLYQNSVLENHWR	248
Db	449	LATPDLDAVPTDLEALFAAATDVDPGVSNQLINTSELLMYNDSEVLMHNHLA	508
Qy	249	STIGHLRESR--LLAHLPKEMTQDIEQOLGSLLATIDINRNQEFITRLKAHLNID---	302
Db	509	VGFKILQEDNCIDFNLNSKRQRQSIRKMDVMDLVAIDMSKHMTLIADLKTMVETKVTSS	568
Qy	303	-LRLDEAQDRHFMQIAALKACDINCPRIWEMSKQWSERVICEFYGROGLEQKFPELEIS	360
Db	569	GVLJJDNYSDPRIQVRNMVHCAUDSNTPKPLELYQWTDTIMAEPQQGDRERGMEIS	628
Qy	361	PLCNQOKDSTPSIQGFMSSIVEPREWAHTFGNSTLSENMLGHIAHNKAQWKSIL---	417
Db	629	PMCDKHTASVEKSQVSGFDIXVHPLWETWADLVHD--AQEILDTELDNRDWYSAIROQ	686
Qy	418	--PRQRHRSRGSSGGG-PDHDHAGGCTESSEQE	446
Db	687	PSPPPBEEESKGPGHPPPLDKPQFELITTLEEEE	719
RESULT 11			
	167946	3', 5'-Cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat	
	N;Alternate names:	cyclic AMP-specific phosphodiesterase R1; RpDE4A1	
	N;Contains:	'3', 5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-specific phosphodiesterase RD3)	
	C;Species:	Rattus norvegicus (Norway rat)	
	C;Date:	29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004	
	C;Accession:	I67946; A32558; B32558; C32558	
	R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.		
	Gene 149, 237-244, 1994		
	A;Title:	Differential CNS expression of alternative mRNA isoforms of the mammalian gene	
	A;Reference number:	I53865; MUID:95047482; PMID:7958936	
	A;Accession:	I67946	
	A;Status:	Translated from GB/EMBL/DBJ	
	A;Molecule type:	mRNA	
	A;Residues:	1-610 <RES>	
	A;Cross-references:	UNIPROT:P54748; UNIPARC:UPI00000246D4; GB:L27062; PIDN:9436613; PIDN:9203984; PIDN:AAA41101.1; PID:R;Davis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.	
	A;Molecule type:	mRNA	
	A;Residues:	85-120,154-598,'T',600-610 <DA2>	
	A;Cross-references:	UNIPARC:UPI0000170939; GB:M26716; GB:N26717; GB:J04554; NID:g203986; A;Note:	
	A;Accession:	C32558	
	A;Molecule type:	mRNA	
	A;Residues:	1-598,'T',600-610 <DAV>	
	A;Cross-references:	UNIPARC:UPI0000170937; GB:M26715; PIDN:9203982; PIDN: AAC37699.1; PID: B32558	
	A;Accession:	B32558	
	A;Cross-references:	UNIPARC:UPI0000170938; GB:M26716; PIDN:9203984; PIDN:AAA41101.1; PID:RD3	
	C;Superfamily:	3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'	
	C;Keywords:	Alternative splicing; cAMP binding; phosphoric diester hydrolase	
	F;14-20/Region:	responsible for membrane association	
	F;26-610/Product:	3', 5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status PR	
	F;85-120,154-610/Product:	3', 5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #status PR	
	F;184-412/Domain:	3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>	
	Query Match	23.2%	Score 559.5; DB 2; Length 610;
	Best Local Similarity	31.1%	Pred. No. 3.9e-36;
	Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;		
Qy	43	RGSYPFIDRLRUMSTSYSCBIGTKVKRLLSFORYFHASRLRGITPQAPLHLIDDEGYI	102
Db	80	RQSQPMQSQTIGLKLVHFTGSLNTN-----VPRFGVKTQDQEDLL	117
Qy	103	GOARHMLSKVGMMDFDIFLFDRLLTGNSLVTLLCHLLENTHGLIHFKEQDMVTLHFLVMV	162

Qy	395	NSTLSENNIGHLAHIKAOKWSSLPRQRHRSRGSSGP-DHDHAGGQ-----TE	441	555	PLYRQMTDRIMAEFFQGDRERESGIDISPMCDCHTPASVEKSQVGFDYIAHPLWETWAD	614
Db	619	PD-AQDLDTLBDRN-DM-----YHSAIRQSPSPPLBEPGLGHPSLPDKFQFELT	699	392	FTGNSTLSENNIGHLAHIKAOKWSSLPRQRHRSRGSSGP-DHDHAGGQ-----TE	443
Qy	442	SEOBEGDS 449		615	LVHPD-AQDLDTLBDRNREMYQSKIPRSPSDLTNRDFQFELTLEFAEEEDSEE	672
Db	700	EEBEEDDS 707		673	EEEGE 677	
RESULT 13						
S71626		3'-5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human		RESULT 14		
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase		C:Species: Homo sapiens (man)		167945	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)	
C;Date: 27-Nov-1997 #text_change 12-Dec-1997 #text_change 09-Jul-2004		N;Alternate names: cAMP phosphodiesterase 1			N;Alternate names: cAMP phosphodiesterase (Norway rat)	
C;Accession: S71626; I61356		C;Species: Rattus norvegicus (Norway rat)			C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004	
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.		C;Accession: I67945; A33904			C;Accession: I67945; A33904	
FEB5 Lett. 305:310, 1995		R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.			R;Swinnen, J.V.; Joseph, D.R.; Conti, M.	
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific gene		Gene 149, 237-244, 1994			Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989	
A;Reference number: S71626; MUID:95145731; PMID:7843419		A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes			A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce gene	
A;Accession: S71626		A;Reference number: 153865; MUID:958996; PMID:958996			A;Reference number: A33904; MUID:89315790; PMID:2546153	
A;Molecule type: DNA		A;Accession: I67945			A;Accession: A33904	
A;Residues: 1-712 <ENG>		A;Status: preliminary; translated from GB/EMBL/DDBJ			A;Status: preliminary	
A;Cross-references: UNIPROT:Q08493; UNIPARC:UPI0000163B31; EMBL:Z46632; PID:5727222; PID:167945		A;Molecule type: mRNA			A;Molecule type: mRNA	
A;Experimental source: substantia nigra		A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:208410			A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:208410	
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993		C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene			C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene	
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory gene		C;Keywords: alternative splicing; cAMP binding; phosphotriesterase homology <CNPD>			C;Keywords: alternative splicing; cAMP binding; phosphotriesterase homology <CNPD>	
A;Reference number: A54442; MUID:94019330; PMID:8413254		F:387-615;/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homologous to the dunce learning and memory gene			F:253-481;/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homologous to the dunce learning and memory gene	
A;Accession: I61356		A;Status: preliminary; translated from GB/EMBL/DDBJ			A;Status: preliminary	
A;Molecule type: mRNA		A;Accession: I61356			A;Molecule type: mRNA	
A;Residues: 462-712 <RES>		A;Cross-references: UNIPARC:UPI000016AE86; GB:L20968; PID:9347125; PID:AAA03591.1; PID:167945			A;Cross-references: UNIPARC:UPI000016AE86; GB:L20968; PID:9347125; PID:AAA03591.1; PID:167945	
C;Genetics:		C;Function:			C;Function:	
C;Gene: HSPDE4 C1		A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP			A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP	
C;Pathway: cyclic nucleotide metabolism		A;Note: expressed in various tissues but not in cells of the immune system			A;Note: expressed in various tissues but not in cells of the immune system	
C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene		A;Note: expressed in various tissues but not in cells of the immune system			A;Note: expressed in various tissues but not in cells of the immune system	
F:387-615;/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homologous to the dunce learning and memory gene		C;Keywords: alternative splicing; cAMP binding; phosphotriesterase homology <CNPD>			C;Keywords: alternative splicing; cAMP binding; phosphotriesterase homology <CNPD>	
Query Match Score 553; DB 2; Length 712;		Best Local Similarity 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;			Query Match Score 529.5; DB 2; Length 536;	
Matches 135; Conservative 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;		Best Local Similarity 30.8%; Pred. No. 7.5e-34; Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;			Best Local Similarity 30.8%; Pred. No. 7.5e-34; Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;	
Qy	11	EILFENPDQNAKCVCMGLDPIRLRGCTGTYRAERRGSYPFDRLIN-----STYSG-	61	Qy	71 RLLSFQRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	130
Db	204	KLAETLDELWDICDQLETIQLTRHSGVEMNSKFK-----RINRLETHLSETSRSGNQ	257	Db	156 QTIGIRKSCTS-LPTAAIPFGVQDQEEPLAKE--LEPTNRKGIDVFRVAFELSGNRP	211
Qy	62	-----BIGMK-----KVTKRLSFRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	99	Qy	131 LVTLLCHLFNTGHGLIHFKLDMVTLHRELWVQDYSQHSONPYHNAVHAADYVQAMCYLK	190
Db	258	VSEYISRTFLDQQTTEVELPKVTAEEAQMSRISGLHGHCHSASLSATTVPREFGQDPOE	317	Db	212 LTAVTFRVQLQERDLKLTQFQIPADTLKLTLEGHYHSNAYVQSAHVLQG	271
Qy	100	DYLGQARANMISKVGMWDPPDFLFLDRLTNSLSVTLCHLFIATHLHIFKLDVNLTHREL	159	Qy	191 BPKLASFPLTDIMIGLLAANAHDVPHGYNQPLFLKTKHNLQNMSLLENHFRST	250
Db	318	EQLAKE--LEDTNKGWLQDVKYADVSGNRPITAIIFSPQERDLKLTQFQIPADTLKLT	374	Db	272 TPALAEVFTDLEVAIAIFACAIHDVDPGVSQNQELINTSELALMYNDSSVLENHHLAVG	331
Qy	160	VNPFLIITNHHLANLYQNMSSVLENHWRSTIGMRESR--LLAHLPKEMTQDIEQQLGS	277	Qy	251 IGMRLRSR--LLAHLPKEMTQDIEQQLGSLLATDINRNEFLTRIKAHLINKD-----	302
Db	435	VSNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422	Db	332 FRLQJENCDIPQNUISTRQKLSLRANVIDNLATNSKRSLLADIKTIVETKRTVLSGV	391
Qy	278	LILATDINRQEFLTRIKAHLINKD-----LRJBDADPRHFMQIALKCADICNPCTRIM	494	Qy	303 LRLEDAAQDHFMQLQIALKCADICNPCTRIM	362
Db	495	MVLATDMSKHMNLILLAKTMVKEKKVTSUQLLDDNYSRDIQVQLNVLCAQDSNPNTPL	554	Db	392 LLDDNTSDRITQVLQSLVHCAQDLSNPNTPL	451
Qy	442	444 EOEQD 448		Qy	363 CNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422
Db	673	EEEGE 677		Db	452 CDKHTASVEKSQVGFDYIAHPLWETWADLVHPD-AQELLDTLEDRNREWYQSRV-----	505
RESULT 14						
S71626		3'-5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human			506 CSPPHAIQGDPRFKETITLEETEEEEEDE	534
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase		C:Species: Homo sapiens (man)				
C;Date: 27-Nov-1997 #text_change 12-Dec-1997 #text_change 09-Jul-2004		N;Alternate names: cAMP phosphodiesterase 1				
C;Accession: S71626; I61356		C;Species: Rattus norvegicus (Norway rat)				
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.		C;Accession: I67945; A33904				
FEB5 Lett. 305:310, 1995		R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.				
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific gene		Gene 149, 237-244, 1994				
A;Reference number: S71626; MUID:95145731; PMID:7843419		A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes				
A;Accession: S71626		A;Reference number: 153865; MUID:958996; PMID:958996				
A;Molecule type: DNA		A;Accession: I67945				
A;Residues: 1-712 <ENG>		A;Status: preliminary; translated from GB/EMBL/DDBJ				
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A;Experimental source: substantia nigra		A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:208410				
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993		C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene				
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory gene		C;Keywords: alternative splicing; cAMP binding; phosphotriesterase homology <CNPD>				
A;Reference number: A54442; MUID:94019330; PMID:8413254		F:387-615;/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homologous to the dunce learning and memory gene				
A;Accession: I61356		A;Status: preliminary; translated from GB/EMBL/DDBJ				
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C;Genetics:		C;Function:				
C;Gene: HSPDE4 C1		A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP				
C;Pathway: cyclic nucleotide metabolism		A;Note: expressed in various tissues but not in cells of the immune system				
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Query Match Score 553; DB 2; Length 712;		Best Local Similarity 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;				
Matches 135; Conservative 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;		Best Local Similarity 30.8%; Pred. No. 7.5e-34; Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;				
Qy	11	EILFENPDQNAKCVCMGLDPIRLRGCTGTYRAERRGSYPFDRLIN-----STYSG-	61	Qy	71 RLLSFQRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	130
Db	204	KLAETLDELWDICDQLETIQLTRHSGVEMNSKFK-----RINRLETHLSETSRSGNQ	257	Db	156 QTIGIRKSCTS-LPTAAIPFGVQDQEEPLAKE--LEPTNRKGIDVFRVAFELSGNRP	211
Qy	62	-----BIGMK-----KVTKRLSFRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	99	Qy	131 LVTLLCHLFNTGHGLIHFKLDMVTLHRELWVQDYSQHSONPYHNAVHAADYVQAMCYLK	190
Db	258	VSEYISRTFLDQQTTEVELPKVTAEEAQMSRISGLHGHCHSASLSATTVPREFGQDPOE	317	Db	212 LTAVTFRVQLQERDLKLTQFQIPADTLKLTLEGHYHSNAYVQSAHVLQG	271
Qy	100	DYLGQARANMISKVGMWDPPDFLFLDRLTNSLSVTLCHLFIATHLHIFKLDVNLTHREL	159	Qy	191 BPKLASFPLTDIMIGLLAANAHDVPHGYNQPLFLKTKHNLQNMSLLENHFRST	250
Db	318	EQLAKE--LEDTNKGWLQDVKYADVSGNRPITAIIFSPQERDLKLTQFQIPADTLKLT	374	Db	272 TPALAEVFTDLEVAIAIFACAIHDVDPGVSQNQELINTSELALMYNDSSVLENHHLAVG	331
Qy	160	VNPFLIITNHHLANLYQNMSSVLENHWRSTIGMRESR--LLAHLPKEMTQDIEQQLGS	277	Qy	251 IGMRLRSR--LLAHLPKEMTQDIEQQLGSLLATDINRNEFLTRIKAHLINKD-----	302
Db	435	VSNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422	Db	332 FRLQJENCDIPQNUISTRQKLSLRANVIDNLATNSKRSLLADIKTIVETKRTVLSGV	391
Qy	278	LILATDINRQEFLTRIKAHLINKD-----LRJBDADPRHFMQIALKCADICNPCTRIM	494	Qy	303 LRLEDAAQDHFMQLQIALKCADICNPCTRIM	362
Db	495	MVLATDMSKHMNLILLAKTMVKEKKVTSUQLLDDNYSRDIQVQLNVLCAQDSNPNTPL	554	Db	392 LLDDNTSDRITQVLQSLVHCAQDLSNPNTPL	451
Qy	442	444 EOEQD 448		Qy	363 CNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422
Db	673	EEEGE 677		Db	452 CDKHTASVEKSQVGFDYIAHPLWETWADLVHPD-AQELLDTLEDRNREWYQSRV-----	505
RESULT 14						
S71626		3'-5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human				
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase		C:Species: Homo sapiens (man)				
C;Date: 27-Nov-1997 #text_change 12-Dec-1997 #text_change 09-Jul-2004		N;Alternate names: cAMP phosphodiesterase 1				
C;Accession: S71626; I61356		C;Species: Rattus norvegicus (Norway rat)				
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.		C;Accession: I67945; A33904				
FEB5 Lett. 305:310, 1995		R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.				
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific gene		Gene 149, 237-244, 1994				
A;Reference number: S71626; MUID:95145731; PMID:7843419		A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes				
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A;Molecule type: DNA		A;Accession: I67945				
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A;Experimental source: substantia nigra		A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:208410				
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993		C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene				
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C;Genetics:		C;Function:				
C;Gene: HSPDE4 C1		A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP				
C;Pathway: cyclic nucleotide metabolism		A;Note: expressed in various tissues but not in cells of the immune system				
C;Superfamily: 3', 5'-cyclic nucleotide phosphodiesterase homologous to the dunce learning and memory gene		A;Note: expressed in various tissues but not in cells of the immune system				
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Query Match Score 553; DB 2; Length 712;		Best Local Similarity 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;				
Matches 135; Conservative 27.8%; Pred. No. 1.6e-35; Matches 94; Mismatches 198; Indels 58; Gaps 10;		Best Local Similarity 30.8%; Pred. No. 7.5e-34; Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;				
Qy	11	EILFENPDQNAKCVCMGLDPIRLRGCTGTYRAERRGSYPFDRLIN-----STYSG-	61	Qy	71 RLLSFQRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	130
Db	204	KLAETLDELWDICDQLETIQLTRHSGVEMNSKFK-----RINRLETHLSETSRSGNQ	257	Db	156 QTIGIRKSCTS-LPTAAIPFGVQDQEEPLAKE--LEPTNRKGIDVFRVAFELSGNRP	211
Qy	62	-----BIGMK-----KVTKRLSFRYFHASRLRLGIITPAFLHLDDEYLQGARHMLSKVGMMDIFIFPDLRTNGNS	99	Qy	131 LVTLLCHLFNTGHGLIHFKLDMVTLHRELWVQDYSQHSONPYHNAVHAADYVQAMCYLK	190
Db	258	VSEYISRTFLDQQTTEVELPKVTAEEAQMSRISGLHGHCHSASLSATTVPREFGQDPOE	317	Db	212 LTAVTFRVQLQERDLKLTQFQIPADTLKLTLEGHYHSNAYVQSAHVLQG	271
Qy	100	DYLGQARANMISKVGMWDPPDFLFLDRLTNSLSVTLCHLFIATHLHIFKLDVNLTHREL	159	Qy	191 BPKLASFPLTDIMIGLLAANAHDVPHGYNQPLFLKTKHNLQNMSLLENHFRST	250
Db	318	EQLAKE--LEDTNKGWLQDVKYADVSGNRPITAIIFSPQERDLKLTQFQIPADTLKLT	374	Db	272 TPALAEVFTDLEVAIAIFACAIHDVDPGVSQNQELINTSELALMYNDSSVLENHHLAVG	331
Qy	160	VNPFLIITNHHLANLYQNMSSVLENHWRSTIGMRESR--LLAHLPKEMTQDIEQQLGS	277	Qy	251 IGMRLRSR--LLAHLPKEMTQDIEQQLGSLLATDINRNEFLTRIKAHLINKD-----	302
Db	435	VSNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422	Db	332 FRLQJENCDIPQNUISTRQKLSLRANVIDNLATNSKRSLLADIKTIVETKRTVLSGV	391
Qy	278	LILATDINRQEFLTRIKAHLINKD-----LRJBDADPRHFMQIALKCADICNPCTRIM	494	Qy	303 LRLEDAAQDHFMQLQIALKCADICNPCTRIM	362
Db	495	MVLATDMSKHMNLILLAKTMVKEKKVTSUQLLDDNYSRDIQVQLNVLCAQDSNPNTPL	554	Db	392 LLDDNTSDRITQVLQSLVHCAQDLSNPNTPL	451
Qy	442	444 EOEQD 448		Qy	363 CNQDSDISIPIQIGPMSYIVEPFLFREWAAHPTGNSTLSENNLGHJLANKRAQKNSLLPQRH	422
Db	673	EEEGE 677		Db	452 CDKHTASVEKSQVGFDYIAHPLWETWADLVHPD-AQELLDTLEDRNREWYQSRV-----	505
RESULT 14						
S71626		3'-5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human				
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase		C:Species: Homo sapiens (man)				
C;Date: 27-Nov-1997 #text_change 12-Dec-1997 #text_change 09-Jul-2004		N;Alternate names: cAMP phosphodiesterase 1				
C;Accession: S71626; I61356		C;Species: Rattus norvegicus (Norway rat)				
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.		C;Accession: I67945; A33904				
FEB5 Lett. 305:310, 1995		R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.				
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific gene		Gene 149, 237-244, 1994				
A;Reference number: S71626; MUID:95145731; PMID:7843419		A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes				
A;Accession: S71626						

RESULT 15

T16769 hypothetical protein R153.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T16769

R;Kirsteen, J.

submitted to the EMBL Data Library, June 1995

A;Description: The sequence of C. elegans cosmid R153.

A;Reference: Z18573

A;Accession: T16769

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-549 <KIR>

A;Cross-references: UNIPROT:Q22000; UNIPARC:UPI000013CD8; EMBL:U28729; NID:9861238; PID:

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP-R153.1

A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5' P;281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

C;Genetics:

A;Residues: 1-549 <KIR>

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A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP-R153.1

A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5' P;281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match, Similarity 32.6%; Pred. No. 7.5e-31;

Matches 114; Conservative 72; Mismatches 140; Indels 24; Gaps 6;

Score 517; DB 2; Length 549;

Best Local Similarity 21.5%;

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Om protein - protein search, using sw model

Run on: March 10, 2006, 19:52:25 ; Search time 187.805 Seconds
 (without alignments)

1690.519 Million cell updates/sec

Title: US-10-781-181-5
 Perfect score: 2408
 Sequence: 1 MSCLMVERGEILLEFENPDQN.....EDHDHAGCTTESEQEGDSP 450

Scoring table: BL030662
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database : UniProt_05_80:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2408	PDE7B HUMAN	450	1	PDE7B_HUMAN	Q9NP56	Q9NP56 homo sapien
2	2408	05VWY9 HUMAN	450	2	05VWY9_HUMAN	Q9yv9	05VWY9 homo sapien
3	2258	Q4LB81_HUMAN	586	2	Q4LB81_HUMAN	Q4le81	homo sapien
4	2178	PDE7B_MOUSE	446	1	PDE7B_MOUSE	Q9gkq1	mus musculus
5	2178	08VIB4_RAT	446	1	08VIB4_RAT	Q9vi4	rattus norvegicus
6	2178	08CB52_MOUSE	446	2	08CB52_MOUSE	Q8cb2	mus musculus
7	2161.5	Q8VIB2_RAT	459	2	Q8VIB2_RAT	Q9vie2	rattus norvegicus
8	1764	08VIB3_RAT	359	2	08VIB3_RAT	Q9vie3	rattus norvegicus
9	1510.5	Q4RR95_TETNG	456	2	Q4RR95_TETNG	Q9rr95	tetradon niger
10	1424.5	PDE7A_MOUSE	456	1	PDE7A_MOUSE	Q950m	xenopus laevis
11	1424.5	06PFG2_MOUSE	482	2	06PFG2_MOUSE	Q9D5g2	mus musculus
12	1419.5	PDE7A_HUMAN	482	1	PDE7A_HUMAN	Q9xj46	homo sapien
13	1419.5	Q9SR95_PONPY	456	2	Q9SR95_PONPY	Q9xj5	pongo pygmaeus
14	1397.5	PDE7A_RAT	426	1	PDE7A_RAT	Q98499	homo sapien
15	1287	Q96f72_HUMAN	424	2	Q96f72_HUMAN	Q96f72	homo sapien
16	1267.5	Q4RR95_TETNG	52.6	2	Q4RR95_TETNG	Q4RR95	tetradon niger
17	1107.5	04RFT4_MACRFA	46.0	2	04RFT4_MACRFA	Q4rft4	macaca fasciata
18	872	Q7PNP5_ANOGA	36.2	2	Q7PNP5_ANOGA	Q7Pnp5	anophelis gambiae
19	711	QAYAJ0_HUMAN	29.5	2	QAYAJ0_HUMAN	Q9vxj0	homo sapien
20	604.5	PDE4D_HUMAN	42.1	1	PDE4D_HUMAN	Q98499	homo sapien
21	603.5	PDE4D_RAT	25.1	1	PDE4D_RAT	Q14270	rattus norvegicus
22	600.5	PDB4D_MOUSE	747	2	PDB4D_MOUSE	Q9b4d	mus musculus
23	580.5	Q8VDB1_RAT	24.1	1	Q8VDB1_RAT	Q9vd81	rattus norvegicus
24	580.5	PDE4B_RAT	24.1	1	PDE4B_RAT	Q14646	rattus norvegicus
25	580.5	Q5RKJ0_RAT	24.1	1	Q5RKJ0_RAT	Q9k5j0	rattus norvegicus
26	580.5	Q8VDB2_RAT	24.1	1	Q8VDB2_RAT	Q9vd82	rattus norvegicus
27	579.5	Q4RJ30_TETNG	24.1	2	Q4RJ30_TETNG	Q4rj30	tetradon niger
28	579.5	Q5ZRK6_CHICK	24.0	2	Q5ZRK6_CHICK	Q95kr6	gallus gallus
29	574.5	Q9QX17_MOUSE	23.9	2	Q9QX17_MOUSE	Q9gx17	mus musculus
30	573.5	Q6IQY6_MOUSE	23.8	2	Q6IQY6_MOUSE	Q9iqy6	mus musculus
31	573.5	Q9IVY2_MOUSE	23.8	2	Q9IVY2_MOUSE	Q9ivy2	mus musculus

RESULT 1
 PDE7B_HUMAN
 ID PDE7B_HUMAN
 AC Q9NP56;
 STANDARD; PRT; 450 AA.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE CAMP-specific 3', 5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
 Name=pDE7B;
 OS Homo sapiens (Human).
 RA Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TAXID=9606;
 RN [1];
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE;Brain;
 RX MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;
 RA Sasaki T., Kotera J., Yuasa K., Omori K.;
 RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase.";
 RL Biochem. Biophys. Res. Commun. 271:1575-583(2000).
 RN [2];
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE;Brain;
 RX MEDLINE=2029226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
 RA Gardner C.B., Robas N.M., Cawkill D., Flidock M.D.;
 RT "Cloning and characterisation of the human and mouse PDE7B, a novel CAMP-specific nucleotide phosphodiesterase.";
 RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
 RN [3];
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
 RC TISSUE;Brain;
 RX MEDLINE=12477732; PubMed=12477732; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Zeeberg B., Buetow K.H., Shemesh C.M., Schuler G.D., Krausser R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Gardner C.B., Flidock M.D., Altschul S.F., Zeeberg B., Buetow K.H., Shemesh C.M., Schuler G.D., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Diatchenko L., Marsuska K., Farmer A.A., Rubin R.A., Rubin G.M., Hong L., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Zeeberg B., Buetow K.H., Shemesh C.M., Schuler G.D., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., 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Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Blaustein A., Peters G.J., Abramson R.D., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X.,

CC	- activity and cAMP metabolism in the brain.	Db	421 HRSRGSSGSGPDPDHAGGTSEEQGDSP 450
CC	- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O = adenosine 5'-phosphate.		
CC	- COFACTOR: Divalent cations (By similarity).		
CC	- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.		
CC	- Insensitive to zaprinast, rolipram, and milrinone.		
CC	- PATHWAY: Cyclic nucleotide metabolism.		
CC	- PROTEIN SUBUNIT: Cyclic nucleotide-gated channel protein.		
CC	- TISSUE: Highly expressed in brain. Also expressed in heart, liver, skeletal muscle, and pancreas.		
CC	- DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.		
CC	- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.		
CC	Ensembl: AB038040; BAA9537.1; - mRNA.	RA	Thomas D.; RA
DR	EMBL: AJ251860; CAB92441.1; - mRNA.	RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BC075082; AAH75082.1; - mRNA.	RN	[2]
DR	EMBL: BC075083; AAH75083.1; - mRNA.	RP	NUCLEOTIDE SEQUENCE.
DR	PIR: JC7266; JCT266.	RA	Williams S.;
DR	PDB: 1LWX; Model: A=104-433.	RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR	Ensembl: ENSG00000171408; Homo sapiens.	RN	[3]
DR	HGNC: HGNC:8792; PDE7B.	RP	NUCLEOTIDE SEQUENCE.
DR	MIM: 604645; -	RA	Cobley V.;
DR	GO: GO:0004115; P: cAMP-specific phosphodiesterase activity; TAS.	RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR	GO: GO:0007165; P: signal transduction; TAS.	DR	EMBL: AL360178; CAH73075.1; - Genomic DNA.
DR	GO: GO:0007268; P: synaptic transmission; TAS.	DR	EMBL: AL38828; CAH95287.1; - Genomic DNA.
DR	InterPro: IPR002073; PDEase.	DR	EMBL: AL133319; CAH73332.1; - Genomic DNA.
DR	Pfam: PF00233; PDEase_I; 1.	DR	EMBL: AL133319; CAH73075.1; JOINED; Genomic DNA.
DR	PRINTS: PR00387; PDIESTERASE_1.	DR	EMBL: AL138828; CAH73332.1; JOINED; Genomic DNA.
DR	PROSITE: PS00126; PDIASE_I; 1.	DR	EMBL: AL133319; CAH95287.1; JOINED; Genomic DNA.
KW	3D-STRUCTURE: cAMP; Hydroxylase.	DR	EMBL: AL360178; CAH95287.1; JOINED; Genomic DNA.
PT	REGION: 172-410 Catalytic (By Similarity).	DR	EMBL: AL133319; CAH73075.1; JOINED; Genomic DNA.
SEQUENCE	450 AA; 51835 MW; EC142BF3B228D0228 CRC64;	DR	Ensembl: ENSG00000171408; Homo sapiens.
DR	MIM: 604645; -	DR	GO: GO:0004114; F: 3'-5'-cyclic-nucleotide phosphodiesterase activity; IEA.
DR	GO: GO:0007165; P: signal transduction; IEA.	DR	GO: GO:0007165; P: catalytic activity; IEA.
DR	GO: GO:0007268; P: synaptic transmission; IEA.	DR	InterPro: IPR00607; Met_phos_hydro.
DR	InterPro: IPR002073; PDEase.	DR	PRINTS: PR00387; PDIESTERASE_1.
DR	SMARF: SM00471; HDC_1.	DR	PROSITE: PS00126; PDEASE_I; 1.
SQ	SEQUENCE: 450 AA; 51835 MW; EC142BF3B228D0228 CRC64;	DR	SEQUENCE: 450 AA; 51835 MW; EC142BF3B228D0228 CRC64;
Query	Query Match Score: 2408; DB: 1; Length: 450; Best Local Similarity: 100.0%; Pred. No. 3..3e-178; Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query	Query Match Score: 2408; DB: 2; Length: 450; Best Local Similarity: 100.0%; Pred. No. 3..3e-178; Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MSCLMVERCGBILFENPDQNAKCVCMGLDIDLQGTVARRGSYFPIDFLRLNSTTYS 60	Qy	1 MSCLMVERCGBILFENPDQNAKCVCMGLDIDLQGTVARRGSYFPIDFLRLNSTTYS 60
Db	1 MSCLMVERCGBILFENPDQNAKCVCMGLDIDLQGTVARRGSYFPIDFLRLNSTTYS 60	Db	1 MSCLMVERCGBILFENPDQNAKCVCMGLDIDLQGTVARRGSYFPIDFLRLNSTTYS 60
Qy	61 GBIGTKKKVKRLLSFQRYFHASRLJGIIQPOAPHLIDEDYLQGARHMLSKVGMWDFDIF 120	Qy	61 GBIGTKKKVKRLLSFQRYFHASRLJGIIQPOAPHLIDEDYLQGARHMLSKVGMWDFDIF 120
Db	61 GBIGTKKKVKRLLSFQRYFHASRLJGIIQPOAPHLIDEDYLQGARHMLSKVGMWDFDIF 120	Db	61 GBIGTKKKVKRLLSFQRYFHASRLJGIIQPOAPHLIDEDYLQGARHMLSKVGMWDFDIF 120
Qy	121 LFDRLTNGSLVTLCHLFNTHGLIHFKLDMDYTLHRFMVLVQDYHSONPYHNAHAAD 180	Qy	121 LFDRLTNGSLVTLCHLFNTHGLIHFKLDMDYTLHRFMVLVQDYHSONPYHNAHAAD 180
Db	121 LFDRLTNGSLVTLCHLFNTHGLIHFKLDMDYTLHRFMVLVQDYHSONPYHNAHAAD 180	Db	121 LFDRLTNGSLVTLCHLFNTHGLIHFKLDMDYTLHRFMVLVQDYHSONPYHNAHAAD 180
Qy	181 VTQAMHCYCLKEPKLASFPLTDIMLGLLAAAHDDVHPGYNQPFLLKTNHNLANYQNMS 240	Qy	181 VTQAMHCYCLKEPKLASFPLTDIMLGLLAAAHDDVHPGYNQPFLLKTNHNLANYQNMS 240
Db	181 VTQAMHCYCLKEPKLASFPLTDIMLGLLAAAHDDVHPGYNQPFLLKTNHNLANYQNMS 240	Db	181 VTQAMHCYCLKEPKLASFPLTDIMLGLLAAAHDDVHPGYNQPFLLKTNHNLANYQNMS 240
Qy	241 VLENHWRSTIGMLRESRLLAHLPKEMTDQEQQLSLLATDNRQNEFLTRKHLIN 300	Qy	241 VLENHWRSTIGMLRESRLLAHLPKEMTDQEQQLSLLATDNRQNEFLTRKHLIN 300
Db	241 VLENHWRSTIGMLRESRLLAHLPKEMTDQEQQLSLLATDNRQNEFLTRKHLIN 300	Db	241 VLENHWRSTIGMLRESRLLAHLPKEMTDQEQQLSLLATDNRQNEFLTRKHLIN 300
Qy	301 KDLRLEDAQRHFMLOIAALKCADCINCPRLWMSKWSOWSERVICEEFYRQGLEQKPELEIS 360	Qy	301 KDLRLEDAQRHFMLOIAALKCADCINCPRLWMSKWSOWSERVICEEFYRQGLEQKPELEIS 360
Db	301 KDLRLEDAQRHFMLOIAALKCADCINCPRLWMSKWSOWSERVICEEFYRQGLEQKPELEIS 360	Db	301 KDLRLEDAQRHFMLOIAALKCADCINCPRLWMSKWSOWSERVICEEFYRQGLEQKPELEIS 360
Qy	361 PLCNQQKQDSSEPSIQTGEMSYIVEPLPREWAFTGNSTLSNMGLAHLNAQWSLLPRO 420	Qy	361 PLCNQQKQDSSEPSIQTGEMSYIVEPLPREWAFTGNSTLSNMGLAHLNAQWSLLPRO 420
Db	361 PLCNQQKQDSSEPSIQTGEMSYIVEPLPREWAFTGNSTLSNMGLAHLNAQWSLLPRO 420	Db	361 PLCNQQKQDSSEPSIQTGEMSYIVEPLPREWAFTGNSTLSNMGLAHLNAQWSLLPRO 420
Qy	421 HRSRGSSGSGPDPDHAGGTSEEQGDSP 450	Qy	421 HRSRGSSGSGPDPDHAGGTSEEQGDSP 450

Db	241	VLENHHWRSTIGMLRRESLIAHLPPREMTQDIEQQQLGSLLATDINRQNNEFLTRKAHLIN	300	Qy	448	DSP 450
Qy	301	KDLRLDEAQDRHFMQLQIALKCADICNPRCWEMSKQNSERVICEEFPYRGCELEQKPELEIS	360	Db	584	DSP 586
Db	301	KDLRLDEAQDRHFMQLQIALKCADICNPRCWEMSKQNSERVICEEFPYRGCELEQKPELEIS	360			
Qy	361	PLCNQQKDSIPIQTSIQIGFMSTIVEPLFREWAHTFGNSTLSENMLGHLAHNAQWKSLLPQ	420			
Db	361	PLCNQQKDSIPIQTSIQIGFMSTIVEPLFREWAHTFGNSTLSENMLGHLAHNAQWKSLLPQ	420			
Qy	421	HRSRGSSSGPDPDHAGQTESEEQGDSP	450			
Db	421	HRSRGSSSGPDPDHAGQTESEEQGDSP	450			
Qy	421	HRSRGSSSGPDPDHAGQTESEEQGDSP	450			
Db	421	HRSRGSSSGPDPDHAGQTESEEQGDSP	450			
RESULT 3						
ID	Q4LBB1_HUMAN PRELIMINARY;	PRT;	586 AA.			
AC	Q4LBB1;					
DT	13-SEP-2005 (TREMBlrel. 31, Created)					
DT	13-SEP-2005 (TREMBlrel. 31, Last sequence update)					
DE	PDE7B variant protein (Pragment).					
GN	Name-PDE7B variant protein;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
NCBI_TAXID	9606;					
OX						
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Brain.					
RA	Nakajima D., Saito K., Yamakawa H., Kikuno R. F., Nakayama M., Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.; "Preparation of a set of expression-ready clones of mammalian long cDNAs encoding large proteins by the ORF trap cloning method.";					
RT	Submitted (MAR-2005) to the EMBL/GenBank/DBJU databases.					
RL	EMBL: AB209990; BAE06072.1; -; mRNA.					
FT	NON_TER 1_1					
SQ	SEQUENCE 586 AA; 66230 MW; F964F0549AFF8D CRC64;					
Qy	Query Match Score 2258; DB 2; Length 586; Best Local Similarity 100.0%; Pred. No. 2e-166; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Db	164	GDIRLHQGTGRAERGSYPFDRLINNTSYGBGTKEKKVRLISFQYFHASRLRG	223			
Qy	88	TIPQAPLHLDDEDYLQARAHMLSKVGMWDFFDIFLFLDRLTGNSLVTLCHLFNTHGLIH	147			
Db	224	IIPOAIPHLLDDEDYLQARAHMLSKVGMWDFFDIFLFLRTGNSLVTLCHLFNTHGLIH	283			
Qy	148	PKLDMLTLLRFLVMQEDTHSONPYNAVHADYQAMMCYLKEPKLASLTPDLMGL	207			
Db	284	PKLDMLTLLRFLVMQEDTHSONPYNAVHADYQAMMCYLKEPKLASLTPDLMGL	343			
Qy	208	LAAAHDVDHPGVNQFLIKTNHHLANLYQNMVSLENHNHRSTGMLQALKCADICNP	267			
Db	344	LAAAHDVDHPGVNQFLIKTNHHLANLYQNMVSLENHNHRSTGMLQALKCADICNP	403			
Qy	268	TQDIEQQLGSLLATDINRQNNEFLTRKAHLHNKDLRLEDQDRHFMQLQALKCADICNP	327			
Db	404	TQDIEQQLGSLLATDINRQNNEFLTRKAHLHNKDLRLEDQDRHFMQLQALKCADICNP	463			
Qy	328	CRIWENSKQNSERVICEBFYRGCELEQKPELEISPLQNOQDSIPSITQIGMMSYIVPLR	387			
Db	464	CRIWENSKQNSERVICEBFYRGCELEQKPELEISPLQNOQDSIPSITQIGMMSYIVPLR	523			
Qy	388	EWAHFTGNSTSSENMLGHLAHNAQWKSLLPQRHRGSSGSPDHAGGTSEEOBG	447			
Db	524	EWAHFTGNSTSSENMLGHLAHNAQWKSLLPQRHSRGSSGSPDHAGGTSEEOBG	583			

Qy 1 MSCINVERCGBILFFNPNDQNAKCVMLGDIRLGGTGVRABERRGSSGYPFDRLINNTYS 60

1	MSCLMVERGEGEVILFESPEOSVKCVCMGLSDVRLRGQTGVPAERGSYPTIDFRLLNNTHS	60
Db		
Qy	61 GETGKCKVKRLLSFQRYFHASLRLRGITPQAPLHLDVQCARAHLSKYGMWDIF 1.20	
Db	61 GETGKCKVKRLLSFQRYFHASLRLRGITPQAPLHLDVQCARAHLSKYGMWDIF 1.20	
Qy	121 LFDRLTNGSLVTLCHLFNTHGLIHHFKLDMVTLHFLVQDLYHQSQPYHNAVHAAD 180	
Db	121 LFDRLTNGSLVTLCHLFNTHGLIHHFKLDMVTLHFLVQDLYHQSQPYHNAVHAAD 180	
Qy	181 VTQAMHCKVKEPKLASFLTRPLDIGHAANAHDDIGNSQPLIKNHHLANLYQMS 240	
Db	181 VTQAMHCKVKEPKLASFLTRPLDIGHAANAHDDIGNSQPLIKNHHLANLYQMS 240	
Qy	241 VLENHHRSTIGMLRESRLAHLPKEMTQDIEQQLSILATDINRNEFLTRLKAHLHN 300	
Db	241 VLENHHRSTIGMLRESRLAHLPKEMTQDIEQQLSILATDINRNEFLTRLKAHLHN 300	
Qy	301 KDLRLEDQDRHMLQIAALKCADICNPRIWENSKWSERVECEFYRQGELEQKFELIS 360	
Db	301 KDLRLEDQDRHMLQIAALKCADICNPRIWENSKWSERVECEFYRQGELEQKFELIS 360	
Qy	361 PLCNCQKDSIPTSIQGFMSIVTEPLPREWAHTGNSTLSENNMLGHIAHNKAQWKSLLPRO 420	
Db	361 PLCNCQKDSIPTSIQGFMSIVTEPLPREWAHTGNSTLSENNMLGHIAHNKAQWKSLLPRO 420	
Qy	421 HRRRGSSSGPDDHAGGTSESSQ_EGDSP 450	
Db	421 HRRRGSSG----QDPAGTAPTELQETGATP 446	
RESULT 5	OBVIE4_RAT	PRELIMINARY;
ID	OBVIE4_RAT	PRELIMINARY;
AC		PRT; 446 AA.
DT	01-MAR-2002 (TREMBLrel. 20; Created)	
DT	01-MAR-2002 (TREMBLrel. 20; Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26; Last annotation update)	
DB	Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17).	
GN	Name=Petr7b; Synonyms=RNPDE7B;	
OS	Rattus norvegicus (Rat)	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Rattus.	
NCBI_TaxID=10116;		
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Brain;	
RA	Sasaki T., Kotera J., Omori K. i.	
RL	Submitted (MAR-2001) to the EMBL/Genbank/ DDBJ databases.	
DR	EMBL; AB057409; BAB79637.1; - ; mRNA.	
DR	HSSP; Q08499; LOYN.	
DR	Ensembl; ENSRNOG00000013456; Rattus norvegicus.	
DR	RGD; 621016; Pde-b.	
DR	GO: GO:0004114; F:3-, 5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.	
DR	GO; GO:0016789; P:hydrolate activity; IEA.	
DR	InterPro; IPR003607; Met_phos_hydro.	
DR	PFAM; PF00333; PDBase_1.	
DR	PRINTS; PR00387; PDISSTERASE1.	
DR	SMART; SM00471; HDC_1.	
DR	PROSITE; PS00126; PDBASE_I; UNKNOWN_1.	
DR	Hydrolyase.	
SQ	SEQUENCE: 446 AA; 51475 MW; 01567BDABC905D19 CRC64;	
SQ	Score 2178; DB 2; Length 446;	
Query Match	Best Local Similarity 90.4%; Pred. No. 2.3e-160;	
Matches 409;	Conservative 16; Mismatches 20; Indels 6; Gaps 2;	
1	MSCLMVERGEGEVILFENFDQNAKCVCMGLSDVRLRGQTGVPAERGSYPTIDFRLLNNTHS 60	

QY	108	MLSKVGMWDFDIFLFDRLTNGNSLVTLCLLFNTHGLIHFKLDMVTLHFLVMQEDYH	167
Db	121	MLSKVGMWDFDIFLFDRLTNGNSLVTLCLLFNTHFLNSGLIHFKLDMVTLHFLVMQEDH	180
QY	168	SQNPYHNAYAADDYTOQAHMCYLKEPKLA\$FTPDIMLGIAAAAHDYDHPGYNQPELIK	227
Db	181	GHRPYHNAYAADDYTOQAHMCYLKEPKLA\$FTPDIMLGIAAAAHDYDHPGYNQPELIK	240
QY	228	TNHHLANLYQNM\$YLNENHWRSTIGMLRSRLLAHLPKEMTQDEQQLGSLILATDINQ	287
Db	241	TNHHLANLYQNM\$YLNENHWRSTIGMLRSRLLAHLPKEMTQDEQQLGSLILATDINQ	300
QY	288	NEFLTRKAHHNKDLRLEDAQDRHFMLOTAALKCADICNCRIVEMSKWSERVICEEFYR	347
Db	301	NEFLTRKAHHNKDLRLENIDQDHFMLOQALKCADICNCRIVEMSKWSERVICEEFTR	360
QY	348	QGLEQKEPELEISPLCNQOKDSIISIQ1GMSVYIPEPLREWAHTGNSTISEMIGHA	407
Db	361	QGDLEQKEPELEISPLCNQOKDSIISIQ1GMSVYIPEPLREWAHTGNSTISEMNLHIA	420
QY	408	HNAKAQWKSLLPRQRSSRGSGDPDHAGQGTSEBQ-EGDSP	450
Db	421	HNAKAQWKSLLSNQHRRGSG----QDPRTGTAPEFILEQPEGATP	459
Db	RESULT 9 QBVIE3_RAT ID QBVIE3_RAT PRELIMINARY; PRT; 359 AA.		
AC	QBVIE3_RAT PRELIMINARY; PRT; 359 AA.		
DT	01-MAR-2002 (TREMBLeL 20, Created)		
DT	01-MAR-2002 (TREMBLeL 20, Last sequence update)		
DT	01-MAR-2004 (TREMBLeL 26, Last annotation update)		
DB	Cyclic nucleotide phosphodiesterase 7B3 (BC 3.1.4.17).		
GN	Name=Pie7b; Synonyms=RNPDE7B;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Rattus.		
NCBI_TaxID=10116;			
RN	NUCLEOTIDE SEQUENCE.		
RP	TISSUE-TESTS;		
RC	Sabaki T., Kotera J., Omori K.; to the EMBL/GenBank/DBJ databases.		
RA	Submitted: (MAR-2001) ; DR: BAB79638.1; - ; mRNA.		
RL	EMBL: AB057410; DR: Q08499; 10YN.		
DR	HSSP: 621016; Pdetb_1;		
DR	DR; GO:004114; F:3; '5'-cyclic-nucleotide phosphodiesterase a. . . IEA.		
DR	GO; GO:0016787; F:hydrolyase activity; IEA.		
DR	GO:001765; P:ion transduction; IEA.		
DR	InterPro: IPR003607; Met_phos_hydro.		
DR	InterPro: IPR002073; PDBase.		
DR	PFM; PF0023; Pbase_I; 1.		
DR	PRINTS; PR00387; PDIESTERAS1.		
DR	SMART; SMD0471; HDC; 1.		
DR	PROSITE; PS00126; PDEASE_I; UNKNOWN_1.		
KW	Hydrolyase.		
SQ	SEQUENCE. 359 AA; 41456 MW; OFF72792737CE48A CRC64;		
QY	Query Match Score 73.3%; Score 1764; DB 2; Length 359;		
Best Local Similarity 92.0%; Pred. No. 2.3e-128;			
Matches 333; Conservative 7; Mismatches 16; Indels 6; Gaps 2;			
Db	90 POAPLHILDEDYIIGOAREHMLSKVGMWDFDIFLFDRLTNGNSLVTLCLLFNTHGLIHHHK 149		
3	POAPLHILDEDYIIGOAREHMLSKVGMWDFDIFLFDRLTNGNSLVTLCLLFNTHGLIHHHK 62		
QY	150 LDNYTLARFLPVMQEDYHSQNPNPYNAHADVTQAMHCYCLKEPKLASLPTLDIMGLIA 209		
Db	63 LDNYTLARFLPVMQEDYHSQNPNPYNAHADVTQAMHCYCLKEPKLASLPTLDIMGLIA 122		
QY	7 BRCGEELFENPDQNAACVCM-----GDIRL-RGQTGY-RAERGRGSYP 47		
Db	1 QCQGAVLTGFLPVMQEDYHSQNPNPYNAHADVTQAMHCYCLKEPKLASLPTLDIMGLIA 60		

QY 48 FIDFRLLNNTTYSGBI--GTTKCKVYKRLISFQRYFHASRLLRGITIQAP--LHLHLDDEYLG 103
 Db 61 LIDLQVLKESSSQQEVASSTRKVQRQLSQRQYCHASRLLRGIVPHAPSILHLDDGYLG 120
 QY 104 QAREHMLSKYGMWDFDIFLFLPDLRTNGNSLTVLCLHLFNTGHGLTHFKLDMVTLHREFLYMVQ 163
 Db 121. QAAHMLSKGTWNDFDIFLFLPDLRTNGNSLTVLCLHLFNTGVLYGLVHFQDLVKLHFLGAKVQ 180
 QY 164 EDYHSQNPNTHAARADTTQAMCYLKKEPKLASKFLTPDLMIGLLARAAMHDIDHPGYNQP 223
 Db 181 EDYHSQNPNTHAARADTTQAMCYLKKEPKLAEQLSPDVFLGUMMAAARAHVDHPGYNQP 240
 Qy 224 FLIKTNHHANLY----QNMSTLENHWRSTIGMLAESRLLAHLPKEMTDIBQQLGS 277
 Db 241 FLIKTRHHLASLIVQHQSQNTSYLESHWRSTIGMLRSGLLSHLPADMSDIBQQLGS 300

QY 278 LILATDINNONEFLTRLKHAKHNKDLRLDAQDRHFMIL-----QIALWK 320
 Db 301 LILATDISSQNNEFLTGFGLHDODLQDLPSSRHFQHAFRSVPAVTCVCCQQTALK 360

QY 321 CADICNPCCRIMWSKOMSERVCEBFYRQCBLEQKFPELTSPLCNQKQDSIPSQIGFMSY 380
 Db 361 CADICNPCCRIMWSKOMSERVCEBFYRQCBLEQKFPELTSPLCDSSRR-LRPALQTGFTSY 419

Qy 381 IVBPLFREVAHTCNSTLBNMIGHLAHKIAQWKL 416
 Db 420 IVBPLFDEHTHRTEFPLSPSLRTMGHLHQNKARNSRL 455

RESULT 10

PDB7A MOUSE STANDARD; PRT; 456 AA.
 AC P70453; Q9ERB3;
 DT 1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE High-affinity cAMP-specific 3', 5'-cyclic phosphodiesterase 7A
 DE (EC 3.1.4.17) (P2A).
 GN Name=Pde7a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarachnoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RC TISSUE=skeletal muscle;
 MEDLINE=97098542; PubMed=8943082; DOI=10.1073/pnas.93.24.14188;
 RA Wang T.-J., Beavo J.A.;
 RT "Identify creation and tissue-specific expression of PDB7 phosphodiesterase splice variants."
 RT PNAS. 93:14188-14192 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RX TISSUE=brain, and Testis;
 MEDLINE=20483661; PubMed=11027622; DOI=10.1006/bbrc.2000.3613;
 RA Wang P., Wu P., Egan R.W., Billah M.M.;
 RT "Cloning, characterization, and tissue distribution of mouse phosphodiesterase 7A1.";
 RL Biochem. Biophys. Res. Commun. 276:1271-1277 (2000).
 CC "- FUNCTION: Plays a role in signal transduction by regulating the intracellular concentration of cyclic nucleotides. This phosphodiesterase is highly specific for cAMP and may have a role in muscle signal transduction.";
 CC "- CATALYTIC ACTIVITY: Adenosine 3', 5'-cyclic phosphate + H(2)O = adenosine 5'-phosphate.
 CC "- COFACTOR: Divalent cations.
 CC "- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
 CC "- PATHWAY: Cyclic nucleotide metabolism.
 CC "- ALTERNATIVE PRODUCTS:
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=PDB7A2;

CC IsoId=P70453-1; Sequence=Displayed;
 CC Name=2; Synonyms=PDE7A1;
 CC IsoId=P70453-2; Sequence=YSP_004594;
 CC TISSUE SPECIFICITY: Widely expressed with highest levels in the skeletal muscle.
 CC DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.
 CC SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.

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CC EMBL: U68171; AAC08479.1; - mRNA.
 DR EMBL; AY07772; AAC16295.1; - mRNA.
 DR HSSP; Q08498; IOTN.
 DR Ensembl; ENSEMBL00000019990; Mus musculus.
 DR MGJ; MGJ:1202402; Pd7a.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR002073; PDBase.
 DR Pfam; PF00233; PDBase.
 DR PRINTS; PRO00387; PDIBSTERASB1.
 DR PRSITE; PS00126; PDBase; I.
 DR VARSPLIC; 1
 FT /FTID=ySP 004594.
 FT A -> D (in Ref. 2).
 ID DR 088268964909F68 CRC64;
 ID DR 59.2%; Score 1425.5; DB 1; Length 456;
 ID DR Best Local Similarity 62.2%; Pred. No. 5.7e-102;
 ID DR Matches 263; Conservative 71; Mismatches 88; Indels 1; Gaps 1;
 ID DR 20 KRGKAISYDSSDOTALYTRMLGDVRVRSRAGFETRGSHPYDRIPHSQDIEASVSA 79
 ID DR 67 KIVKTRLISFQRYFHASRLLRGITIPOAFLHLDDEDYLGQARHMLSKVGMDFDFLFDRLT 126
 ID DR 7 ERGEETLFPENDONAKVCMLGDIRLQGQTGYAERIGSYPFIDFLRLLNSTYSGEGTK 66
 ID DR 80 RNIRRLLISFQYLRISRSRPGATVCSSEDILQDYNGAKCMELKVRWNFDIFLFDLT 139
 ID DR 127 NGNSLVTLLCLHLNTNHGLHFLMTLHLRELVMQEDYHSNQPNYNAHAAADTVQAMH 186
 ID DR 20 KRGKAISYDSSDOTALYTRMLGDVRVRSRAGFETRGSHPYDRIPHSQDIEASVSA 79
 ID DR 140 NGNSLVSUTLFLPSLHGLEYFLDWTMVLKLRPLAVICQEDYHSNQPNYNAHAAADTVQAMH 199
 ID DR 187 CYLKEPLASLFLPLDIMGLLAAAHADVDHPCVNQPLIKTNHHLANLYQNSVSLHENH 246
 ID DR 200 CYLKEPLASLUTPWLISLSTAATHDLDHGCVNQPLIKTNHHLANLYQNSVSLHENH 259
 ID DR 247 WRSTGMGRBSRLLAHLPKEMTQDIEQOLGSLJLATTDINRONEFLTRLKAHLHNKDLRLE 306
 ID DR 260 WRSAGVLLRESGLFSPHPLESQMEAQIGALIATWDISRNQYLSLFRSHLDKGDLHLD 319
 ID DR 307 DAQDRHFMQLQIAKCAADCNCPCRWENSKONSERVECEPYRQGELEQKPELETSPLCNQ 366
 ID DR 320 DGRHRHLVLMQALKACADCNCPCRNWLSKONSEKUTBEFFHQGDIEXCKCYHLYGSPLCBRO 379
 ID DR 367 KDISP1QIGPMSYIVELFREWAFITCNSTLSENNLGHARKQWKSLLPRQRHRSGS 426
 ID DR 380 TESIANIQIGMFTYLVEPLFTEWARPSA-TRUSQTMUGHVGLINKASMKGLQROQPSSED 438

Qy 427 SGS 429
 Db 439 NAA 441

CC throughout development. It persists strongly only in adult skeletal muscle.

CC - I- DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain..

CC - I- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL: L12052; AAB35644.2; -; mRNA.
EMBL: U67932; AAB65772.1; -; mRNA.
DR HSSP; Q08499; I0YN.
DR HGNC; HGNC:8791; PDE7A.
DR MIM; 171185; -.
DR GO; GO:000467; C:cell fraction; NAS.
DR GO; GO:0004115; P:cAMP-specific phosphodiesterase activity; TAS.
DR GO; GO:007165; P:signal transduction; NAS.
DR InterPro; IPR002073; PDEase.
DR PRINTS; PR00387; PDESTERASE1.
DR PROSITE; PS00126; PDEASE I; 1.
DR PROSITE; PS00123; PDEase I; 1.
DR RPRINTS; PR00387; PDESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; UNKNOWN_1.
DR Hypothetical Protein.
SQ SEQUENCE 482 AA; 55505 MW; /FTId=VSP_004593.
SQ SEQUENCE 482 AA; 3B3C8F6E9154F88C CRC64;
Query Match 58.9%; Score 1419.5; DB 1; Length 482;
Best Local Similarity 61.7%; Pred. No. 1.8e-101;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;
QY 7 ERGEIILPFENDPONAKCYOMGLGDLRRLQTGVAERRESYPFDIFRLNNTTYSGEIGTK 66
46 QRGGAISSDSDTALYTRMLGDVRVSRAGFESERRSHPYIDFRFHSQSEIEVVSVA 105
QY 67 KKVKRLLSFQRYPHASRLRGITIPQAPLHLDDEDYLGAHRMILSKVGMWDFDIFLFDRLT 126
: : : : ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 106 RNTRRLLSFQRYLRSRSPRFRTAVNSLNILDDDYNGAOKCMLEKVNWNFDIFLFDRLT 165
QY 127 NGNSLVTLLCHLPLNTKGIIHFFLDLMTLHRFLYMQEDYHSQNPYNAVHAADVTQAMH 186
DB 166 NGNSLVLSTLTHFLSLHGGLIEYFHDMMKLRRFLYMQEDYHSQNPYNAVHAADVTQAMH 225
QY 187 CYLKEPKLASFLTPDLMGLAAAHDDVHPGVNQPLKLTLYKNTSVLENHH 246
DB 200 CYLKEPKLASFLTPDLMGLAAAHDDVHPGVNQPLKLTLYKNTSVLENHH 259
QY 226 CYLKEPKLASFLTPDLMGLAAAHDDVHPGVNQPLKLTLYKNTSVLENHH 285
DB 247 WRSTIGMURESLJAHLPKEMTQDIEQQIGSILATDINRONEFLTRIKAHLNKDLRLE 306
: : : : ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 286 WRSAGVLLRESGLFSHLPIESRQMETOGITALTDISRNEYSLFRSHLDRGDLCLE 345
DB 307 DAQDRHFMQLQALKCADICNPCTIWENSKQWSERVICEFYRCOELBKPELETSPLCNOQ 366
QY 346 DTRHRHLVQMALKCADICNPCTIWENSKQWSERVICEFYRCOELBKPELETSPLCNOQ 405
QY 367 KDSIPISTOIGMSYIVBPLFREWAHTGNCNSTLSENMGHLARKKAWKSLLPRQRHRSRG 426
QY 380 TESIANIQGFMTYLVPLFTEWARFS-NTRLSQTMGLQREQQSSED 438
DB 416 TESTANIQGFMTYLVPLFTEWARFS-NTRLSQTMGLQREQQSSED 464
QY 427 SGS 429
DB 439 DAT 441

Q5R5B5 PONPY PRELIMINARY; PRT; 456 AA.
ID Q5R5B5; PONPY PRELIMINARY; PRT; 456 AA.
AC Q5R5B5; PONPY PRELIMINARY; PRT; 456 AA.
DT 01-FEB-2005 (TRIMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRIMBLrel. 29, Last annotation update)
DT 01-FEB-2005 (TRIMBLrel. 29, Last annotation update)
DE Hypothetical protein DKPZp469BE1731.
Name Name=DKFZp469BE1731;
OS Pongo pygmaeus (Orangutan).
OC Mammalia; Metazoa; Chordata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TISSUE-Kidney;
RG The German cDNA Consortium;
RA Blocker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR860948; CAH93051.1; '-' mRNA.
DR GO; GO:0004114; P:3'-5' -cyclic-nucleotide phosphodiesterase a. . . ; IEA.
DR GO; GO:0016787; P:hydrolyse activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002073; PDEase_I; 1.
DR InterPro; IPR00387; PDEase_I; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
DR Hypothetical Protein.
SQ SEQUENCE 456 AA; 52755 MW; CB162B0BF074BF CRC64;
Query Match 58.9%; Score 1418.5; DB 2; Length 456;
Best Local Similarity 61.7%; Pred. No. 2e-101;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;
QY 7 ERGEIILPFENDPONAKCYOMGLGDLRRLQTGVAERRESYPFDIFRLNNTTYSGEIGTK 66
DB 20 KERGASLYDSSQITALYTRMLGDVRVSRAGFESERRSHPYIDFRFHSQSEIEVVSVA 79
QY 67 KKVKRLLSFQRYPHASRLRGITIPQAPLHLDDEDYLGAHRMILSKVGMWDFDIFLFDRLT 126
DB 80 RNTRRLLSFQRYLRSRSPRFRTAVNSLNILDDDYNGAOKCMLEKVNWNFDIFLFDRLT 139
QY 127 NGNSLVTLLCHLPLNTKGIIHFFLDLMTLHRFLYMQEDYHSQNPYNAVHAADVTQAMH 186
DB 140 NGNSLVLSTLTHFLSLHGGLIEYFHDMMKLRRFLYMQEDYHSQNPYNAVHAADVTQAMH 199
QY 187 CYLKEPKLASFLTPDLMGLAAAHDDVHPGVNQPLKLTLYKNTSVLENHH 246
DB 200 CYLKEPKLASFLTPDLMGLAAAHDDVHPGVNQPLKLTLYKNTSVLENHH 259
QY 247 WRSTIGMURESLJAHLPKEMTQDIEQQIGSILATDINRONEFLTRIKAHLNKDLRLE 306
DB 260 WRSAGVLLRESGLFSHLPIESRQMETOGITALTDISRNEYSLFRSHLDRGDLCLE 319
QY 307 DAQDRHFMQLQALKCADICNPCTIWENSKQWSERVICEFYRCOELBKPELETSPLCNOQ 366
DB 320 DTRHRHLVQMALKCADICNPCTIWENSKQWSERVICEFYRCOELBKPELETSPLCNOQ 379
QY 367 KDSIPISTOIGMSYIVBPLFREWAHTGNCNSTLSENMGHLARKKAWKSLLPRQRHRSRG 426
DB 380 TESIANIQGFMTYLVPLFTEWARFS-NTRLSQTMGLQREQQSSED 438
ID PDE7A_RAT STANDARD; PRT; 426 AA.
RESULT 14

Search completed: March 10, 2006, 20:02:08
Job time : 189,805 SECS

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OM protein - protein search, using sw model 1
Run on: March 10, 2006, 20:02:25 ; Search time 40.8537 Seconds
(without alignments)
910.666 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGBILFFENPDQN.....PDHDEAGQTESEEEQGDSP 450
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Issued_Patents_AA:
1: /cgn2_6/.ptodata/1/iaa/5_COMB.pep*
2: /cgn2_6/.ptodata/1/iaa/6_COMB.pep*
3: /cgn2_6/.ptodata/1/iaa/6_COMB.pep*
4: /cgn2_6/.ptodata/1/iaa/7_COMB.pep*
5: /cgn2_6/.ptodata/1/iaa/8_COMB.pep*
6: /cgn2_6/.ptodata/1/iaa/backfiles1.pep*

Pred. No. is the number of results predicted by chance to have a score greater than or equal 1 to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2258	93.8	502	2	US-09-330-970-1	Sequence 1, Appli
2	2051	85.2	390	2	US-09-949-016-10020	Sequence 10020, A
3	1419.5	58.9	498	1	US-07-688-352C-20	Sequence 20, Appli
4	1419.5	58.9	498	1	US-08-474-379C-20	Sequence 20, Appli
5	1419.5	58.9	498	2	US-09-146-249A-20	Sequence 20, Appli
6	1419.5	58.9	498	2	US-08-206-188B-20	Sequence 20, Appli
7	1280	53.2	320	2	US-09-330-970-3	Sequence 3, Appli
8	604.5	25.1	518	2	US-09-602-735B-2	Sequence 2, Appli
9	604.5	25.1	673	1	US-08-474-379C-63	Sequence 63, Appli
10	604.5	25.1	673	2	US-09-146-249A-63	Sequence 63, Appli
11	604.5	25.1	673	2	US-08-206-188B-63	Sequence 63, Appli
12	603.5	25.1	517	2	US-09-602-735B-4	Sequence 4, Appli
13	599.5	24.9	673	1	US-08-577-492-35	Sequence 35, Appli
14	599.5	24.9	673	2	US-09-079-630-35	Sequence 35, Appli
15	580.5	24.1	562	1	US-07-688-352C-4	Sequence 8, Appli
16	580.5	24.1	562	1	US-08-942-521B-8	Sequence 4, Appli
17	580.5	24.1	562	1	US-08-474-379C-4	Sequence 4, Appli
18	580.5	24.1	562	2	US-09-146-249A-4	Sequence 4, Appli
19	580.5	24.1	562	4	PCT-US-94-02714-4	Sequence 4, Appli
20	580.5	24.1	562	2	US-08-206-188B-4	Sequence 4, Appli
21	574.5	23.9	721	2	US-09-983-754-2	Sequence 2, Appli
22	567.5	23.6	564	1	US-08-577-492-34	Sequence 34, Appli
23	567.5	23.6	564	1	US-08-942-521B-2	Sequence 2, Appli
24	567.5	23.6	564	1	US-08-474-379C-59	Sequence 59, Appli
25	567.5	23.6	564	2	US-09-146-249A-59	Sequence 59, Appli
26	567.5	23.6	564	2	US-08-206-188B-59	Sequence 32, Appli
27	567.5	23.6	564	2	US-09-079-630-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-330-970-1
; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; Kappeler-Libermann, Rosana
; TITLE OF INVENTION: Human Cyclic Nucleotide
; TIDE
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: US/09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-1

Query Match 93.8%; Score 2258; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2e-229; Matches 423; Conserv. 0; Missmatches 0; Indels 0; Gaps 0;

QY 28 GD1RLGTGVTGVRARRGSYPPTDFRLANSTTSGEIGKKVYKLSSLORYFHASRLLRG 87
Db 80 GD1RLGTGVTGVRARRGSYPPTDFRLANSTTSGEIGKKVYKLSSLORYFHASRLLRG 139
QY 88 IIPOPAPHLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTGLTH 147
Db 140 IIPOPAPHLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFNTGLTH 199
QY 148 FKLDMDVTLHRFLYIVQEDYHQSOPHYNAHAADYQAMHCYLKEPKLASFPLTDIMLGL 207
Db 260 LAAAHADVDHPGTNQPFLIKTNFHNLANYQNMSVLENHHWRSTGMLRESRLIAHLPKEM 319
QY 268 TDIEQQLGSLLATDINQNFLTAKHLANKDLRLEDQDRHFMQIAALKCADICNP 327
Db 200 FKLDMDVTLHRFLYIVQEDHSQNSYHNAHAADYQAMHCYLKEPKLASFPLTDIMLGL 259
QY 208 LAAAHADVDHPGTNQPFLIKTNFHNLANYQNMSVLENHHWRSTGMLRESRLIAHLPKEM 267
Db 260 LAAAHADVDHPGTNQPFLIKTNFHNLANYQNMSVLENHHWRSTGMLRESRLIAHLPKEM 319
QY 328 CRIWMSKOWSERVCYEFYQGELQEKFELISPLCNQOKDSIPSQIGFMSYTVEPFLFR 387
Db 380 CRIWMSKOWSERVCYEFYQGELQEKFELISPLCNQOKDSIPSQIGFMSYTVEPFLFR 439

Qy 388 EWAHTGNSTLSENLGHLAHNKAQWKSLLPRQRHRSRGSSGPDHDHAGQTESEEQG 447
 Db 440 EWAHTGNSTLSENLGHLAHNKAQWKSLLPRQRHRSRGSSGPDHDHAGQTESEEQG 499

Qy 448 DSP 450
 Db 500 DSP 502

RESULT 2

US-09-949-016-10020 Application US/09949016
 Sequence 10020, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-0

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10020

LENGTH: 390

TYPE: PRT

ORGANISM: Human

US-09-949-016-10020

Query Match 85.2%; Score 2051; DB 2; Length 390;
 Best Local Similarity 92.4%; Pred. No. 6.1e-208; Indels 32; Gaps 1;
 Matches 390; Conservative 0; Mismatches 0;

Qy 29 DIRURGQTGVAERGSYFIDFLNLSNTSYSGIGTRKVKRLLSFYRFHASRLRG 88
 Db 1 DIRURGQTGVAERGSYFIDFLNLSNTSYSGIGTRKVKRLLSFYRFHASRLRG 60

Qy 89 1PQAPLHILDEDYLGQARMLSKVGMWDIDFLPDR1NGNSLVLLCHLENTHGLIHF 148
 Db 61 1PQAPLHILDEDYLGQARMLSKVGMWDIDFLPDR1N----- 99

Query Match 58.9%; Score 1419.5; DB 1; Length 498;
 Best Local Similarity 51.7%; Pred. No. 5.2e-141; Indels 1; Gaps 1;
 Matches 261; Conservative 70; Mismatches 91;

Qy 149 KLDNVTLHRLFLVMQEDYISQNPYTHNAVADYQTMNSVLEHNRSTGMLRSLHLPEMT 208
 Db 100 ----- -VMVQEDYISQNPYTHNAVADYQTMNSVLEHNRSTGMLRSLHLPEMT 148

Qy 209 AAAAHDVDPGVNQPFKLTKHHLANLYCNMSVLEHNRSTGMLRSLHLPEMT 268
 Db 149 AAAAHDVDPGVNQPFKLTKHHLANLYCNMSVLEHNRSTGMLRSLHLPEMT 208

Qy 269 QD15QLGSLLATDINRONEFLTRKALHNKDLRLEDQDRHFMQLQALKCADICNP 328
 Db 209 QD15QLGSLLATDINRONEFLTRKALHNKDLRLEDQDRHFMQLQALKCADICNP 268

Qy 329 RIWEMSKQNSERVICEEFYRQGELEQKFEEIEISPICNQODSIPS1QIGM5TIVEPLRE 388
 Db 269 RIWEMSKQNSERVICEEFYRQGELEQKFEEIEISPICNQODSIPS1QIGM5TIVEPLRE 328

Qy 389 WAHTGNSTLSENLGHLAHNKAQWKSLLPRQRHRSRGSSGSPDHDHAGQTESEOBGD 448
 Db 329 WAHTGNSTLSENLGHLAHNKAQWKSLLPRQRHRSRGSSGSPDHDHAGQTESEOBGD 388

Qy 449 SP 450
 Db 389 SP 390

US-07-688-352C-20
 Sequence 20, Application US/0788352C
 Patent No. 5527896

GENERAL INFORMATION:

APPLICANT: Colicelli, John J.
 TITLE OF INVENTION: Cloning by Complementation and Related Processes
 NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bicknell
 STREET: Two First National Plaza, 20 South Clark Street
 CITY: Chicago
 STATE: Illinois
 COUNTY: USA
 ZIP: 60603

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/688,352C
 FILING DATE: 19910419
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25447

REFERENCE DOCKET NUMBER: 27805/30197

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750
 TELEX: (312) 984-9740
 TELEFAX: 25-3856

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLogy: linear

05-07-688-352C-20

Query Match 58.9%; Score 1419.5; DB 1; Length 498;
 Best Local Similarity 51.7%; Pred. No. 5.2e-141; Indels 1; Gaps 1;
 Matches 261; Conservative 70; Mismatches 91;

Qy 7 ERGGEIIPENPDPQNAKCCVCMGDIRGQTGIVRAERGSYPIDFLRLLNSTYSGGTGT 66
 Db 62 QRGGAISYDSSDOTALYIRMLGDVRARSRAFESERGSHPYIDFRPHQSSEIEVSVA 121

Qy 67 KKVKRLLSFORYFSRHSLLRG1IPOAQLHILDEDYLGQARMLSKVGMWDFDIIFLFDRLT 126
 Db 122 RNIRRLLSFQYLRSLSFSEFRGTAVSSLNLDDYNGQAKCMLKEGVNWNPFLFDRLT 181

Qy 127 NGNSLVTLCLFLNTNGLHHPKLDVTLHRLFLVMQEDYISQNPYTHNAVADYQTMH 186
 Db 182 NGNSLVSLLTFHLSLGLIEYFHLDWMLKLERPLVMQEDYISQNPYTHNAVADYQTMH 241

Qy 187 CYLKEPKLASFLTPD1MGLLAAAHVDHGVNQPLKLNHHHLNLYCNMSVLENNH 246
 Db 242 CYLKEPKLANSUTPWDLSSIAAATHDLDHGVNQPLKLNHYALTYKNTSVLENH 301

Qy 247 WRSTIGMIRESRLLAHLPKENTQDIEQQLGSLIATDINRONEFLTRKALHNKDLRLEDQDRHFMQLQALKCADICNP 328
 Db 302 WRSAVGLRESELLSFHPLSQMETQGAILATDISRONEFLTRKALHNKDLRLEDQDRHFMQLQALKCADICNP 361

Qy 307 DAQDRHEMLQIALKCADCINCPRIWEMSKQNSERVICEEFYRQGELEQKFEEIEISPICNQODSIPS1QIGM5TIVEPLRE 366
 Db 362 DTRHRHVLQWALKCADCINCPRTWELSKQNSERVICEEFYRQGELEQKFEEIEISPICNQODSIPS1QIGM5TIVEPLRE 421

Qy 367 KDSIPSTIQIGFMSYIVBPLFREWAHTGNSLSENNLGHIAHNKAQWKSILPRQHRSRGS 426
 Db 422 TESIANIQQIGMTYLVEPLTTEWAKFS-NTRLSQTMLGHVGLNKASWKRLQLQREOSSSETD 480
 Qy 427 SGS 429
 Db 481 DAA 483

RESULT 4
 US-08-474-379C-20
 ; Sequence 20, Application US/08474379C
 ; Patent No. 5977305
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; COLICELLI, John J.
 ; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
 ; TITLE OF INVENTION: PROCESSES
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,379C
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/688,352
 FILING DATE: 19-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEX/FAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-474-379C-20

Query Match 58.9%; Score 1419.5; DB 1; Length 498;
 Best Local Similarity 61.7%; Pred. No. 5.2e-141; Indels 1; Gaps 1;
 Matches 261; Conservative 70; Mismatches 91;

Qy 7 ERGEETLFENPDQNAKCVCMGDIRURGOTGVRARRGSSPFIDFRLLNSTYSGEIGTK 66
 Db 62 ORRGALSYDSSPQTAIYRMGDVVRSAFESERGRSHYDRIFTSQEDEVSSA 121

Qy 67 KKVKRKLISQFYPHASRLLRGLTIPQAPHLDEDVQAHMLSKVGMMDDFLFDRLT 126
 Db 122 RNIRRRLSFQYRLSSRFERSTAVSNSLNLLDDDTNGQAKCMLKXVNFFNDIFLFDRLT 181

Qy 127 NGNSLVTLCHLFNTNHGLRFLDNVTLHRFLVMQEDYHSQNBYHNAADVTOQAH 186

Db 182 NGNSLVSLSTFHFLFHGLTIEFYHDMICLRRFLVNYIQEYHSONPYHNAADVTOQAH 241
 Qy 187 CYLKPKLANSFLTPLDIMGLLANAHDDHPGNQPLIKTHHLANLYONSVLENH 246
 Db 242 CYLKPKLANSVTPDWLISLIAATHDHPGNQPLIKTHHLATLYKNTSVLENH 301
 Qy 247 WRSTGMRESRLLAHLPKEMTODIEQQLGLSLTADINRNEFLTRUKAHLLNDRLR 306
 Db 302 WRSGAGLIRESGLSPHIFLPSQMMETQGALILTDISRNQELSLFSLHLDQDLCB 361
 Qy 307 DAQDRHEMQLQIALKCADICNPCTIWEMSKWSKSERVCEFYROGPLEBKPKPELEISPLCNQ 366
 Db 362 DTBRHHLVQMALKCADICNPCTIWEMSKWSKSERVTEBFHQDIEKCYHGVSPLCDRH 421
 Qy 367 KDSIPIQIGFMSYIVPLFREWAHTGNSLSENNLGHIAHNKAQWKSILPRQHRSRGS 426
 Db 422 TESIANIQQIGMTYLVEPLTTEWAKFS-NTRLSQTMLGHVGLNKASWKRLQREOSSSETD 480
 Qy 427 SGS 429
 Db 481 DAA 483

RESULT 5
 US-09-146-249A-20
 ; Sequence 20, Application US/09146249A
 ; Patent No. 6069240
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; COLICELLI, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 630 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,249A
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEX/FAX: (312) 474-0448
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 498 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEX: 312-474-0448
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 498 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-146-249A-20

Query Match 58.9%; Score 1419.5; DB 2; Length 498;
 Best Local Similarity 61.7%; Pred. No. 5.2e-141; Indels 1; Gaps 1;
 Matches 261; Conservative 70; Mismatches 91;

Qy 7 ERGEETLFENPDQNAKCVCMGDIRURGOTGVRARRGSSPFIDFRLLNSTYSGEIGTK 66
 Db 62 ORRGALSYDSSPQTAIYRMGDVVRSAFESERGRSHYDRIFTSQEDEVSSA 121

Qy 67 KKVKRKLISQFYPHASRLLRGLTIPQAPHLDEDVQAHMLSKVGMMDDFLFDRLT 126
 Db 122 RNIRRRLSFQYRLSSRFERSTAVSNSLNLLDDDTNGQAKCMLKXVNFFNDIFLFDRLT 181

Qy 127 NGNSLVTLCHLFNTNHGLRFLDNVTLHRFLVMQEDYHSQNBYHNAADVTOQAH 186

Qy 7 ERGGEILFENPDQNAKCVCMIGDIRLRRGGTGTGVRERRGGSYFIDFRLRNLSTTSGEIGTK 66 ; STRANDEDNESS: single
 Db 62 QRGRGATSYSDSDDQTALYIIRMLGDVVRSLRAGFESRRGGSPYDRIFFISQSEEBVSA 121 ; TOPOLOGY: linear
 Molecule type: Protein
 US-08-206-188B-20

Query Match 58.9%; Score 1419.5; DB 2; Length 498;
 Best Local Similarity 61.7%; Pred. No. 5.2e-141;
 Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

Qy 67 KKVKRLLSFQRYFHASRLRGIIQAPLHILDEDYQARHMLSKVGMDFDIFLFDRLT 126 ;
 Db 122 RNIRRLLSFQYLRSSRFQGTAWSNLNLIQMLERGVNNFNDITLFDRLT 181 ;
 Qy 127 NGNSLVTLCLHLNFTHGLIIEYFLDMMKLQRFLMVLTRFLYQDHYSONPYHNAHAADVTQAMH 186 ;
 Db 182 NGNSLVSLTFPLHSLRHGLIEYFLDMMKLQRFLMVLTRFLYQDHYSONPYHNAHAADVTQAMH 241 ;
 Qy 187 CYLKEPKLANSPLTLDIMGLLAAAADHDYDHPGVNPQLIKTKNHLANLYQMSVLENH 246 ;
 Db 242 CYLKEPKLANSVTPDILSLIAAATHDLHPGYNQPLIKTKNHLATLYQMSVLENH 301 ;
 Qy 247 WRSTIGMLRESRLLAHLPLKEMTQDIEQQLGSILATDINRQNEFLTRKALKHLNKDLRE 306 ;
 Db 302 WRSAGVLLRSGSGLFSHPLLESRQOMETOQCALILATDSRQEYLISLFSHLDRGDLCLC 361 ;
 Qy 307 DAQDHFMQLQIAKCADINCPCTRWSKQSERVCCEYPRQGLEQKPELEISPLCNQQ 366 ;
 Db 362 DTRHRHLVLQMALCKACDINCPCTRWSLQSERVCTEEPHQDIEKCYHGLYSPLCDRH 421 ;
 Qy 367 KDSIPSIQIGFMSYIPELFREWRAHTGTNSTLSNMGLHLANKAOKWSLLPROHRSRS 426 ;
 Db 422 TESTANIQIGFMTIVELPLETEWAFS-NTRLSQMLGVGLNKAWSWLQLREBOSSED 480 ;
 Qy 427 SGS 429 ;
 Db 481 DAA 483 ;

RESULT 6
 US-08-206-188B-20 ; Sequence 20, Application US/082061888
 ; Patent No. 6100025
 ; GENERAL INFORMATION:
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.2.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/206,188B
 ; FILING DATE: 01-MAR-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856

Qy 7 ERGCEILFENPDQNAKCVCMIGDIRLRRGGTGTGVRERRGGSYFIDFRLRNLSTTSGEIGTK 66 ;
 Db 62 QRGRGATSYSDSDDQTALYIIRMLGDVVRSLRAGFESRRGGSPYDRIFFISQSEEBVSA 121 ;
 Qy 67 KKVKRLLSFQRYFHASRLRGIIQAPLHILDEDYQARHMLSKVGMDFDIFLFDRLT 126 ;
 Db 122 RNIRRLLSFQYLRSSRFQGTAWSNLNLIQMLERGVNNFNDITLFDRLT 181 ;
 Qy 127 NGNSLVTLCLHLNFTHGLIIEYFLDMMKLQRFLMVLTRFLYQDHYSONPYHNAHAADVTQAMH 186 ;
 Db 182 NGNSLVSLTFPLHSLRHGLIEYFLDMMKLQRFLMVLTRFLYQDHYSONPYHNAHAADVTQAMH 241 ;
 Qy 187 CYLKEPKLANSPLTLDIMGLLAAAADHDYDHPGVNPQLIKTKNHLANLYQMSVLENH 246 ;
 Db 242 CYLKEPKLANSVTPDILSLIAAATHDLHPGYNQPLIKTKNHLATLYQMSVLENH 301 ;
 Qy 247 WRSTIGMLRESRLLAHLPLKEMTQDIEQQLGSILATDINRQNEFLTRKALKHLNKDLRE 306 ;
 Db 302 WRSAGVLLRSGSGLFSHPLLESRQOMETOQCALILATDSRQEYLISLFSHLDRGDLCLC 361 ;
 Qy 307 DAQDHFMQLQIAKCADINCPCTRWSKQSERVCCEYPRQGLEQKPELEISPLCNQQ 366 ;
 Db 362 DTRHRHLVLQMALCKACDINCPCTRWSLQSERVCTEEPHQDIEKCYHGLYSPLCDRH 421 ;
 Qy 367 KDSIPSIQIGFMSYIPELFREWRAHTGTNSTLSNMGLHLANKAOKWSLLPROHRSRS 426 ;
 Db 422 TESTANIQIGFMTIVELPLETEWAFS-NTRLSQMLGVGLNKAWSWLQLREBOSSED 480 ;
 Qy 427 SGS 429 ;
 Db 481 DAA 483 ;

RESULT 7
 US-09-330-970-3
 ; Sequence 3, Application US/093300970
 ; Patent No. 6146876
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; APPLICANT: Kapeller-Liebermann, Rosana
 ; APPLICANT: White, David
 ; TITLE OF INVENTION: A New 6146876 Human Cyclic Nucleotide
 ; FILE REFERENCE: 5800-28
 ; CURRENT APPLICATION NUMBER: US/09/330,970
 ; CURRENT FILING DATE: 1999-06-11
 ; EARLIER APPLICATION NUMBER: 1999-03-23
 ; EARLIER FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 40
 ; SEQ ID NO 3
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-330-970-3

Query Match 53.2%; Score 1280; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.4e-126;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRCQTGTRERRGSYFIDFRLRNLSTTSGEIGTKKKVKRLLSFQYFHASRLRG 87
 Db 80 GDIRLRCQTGTRERRGSYFIDFRLRNLSTTSGEIGTKKKVKRLLSFQYFHASRLRG 139

Query 8B IIPQAPLHLLDBDYLGQARHMLSKVGMWDFDIFLEFDRLTNGNSLVTLCHLFNTHGLIH 147
 Database 140 IIPQAPLHLLDBDYLGQARHMLSKVGMWDFDIFLEFDRLTNGNSLVTLCHLFNTHGLIH 199
 Query 148 FKLDNVTLHRFLVMQEDYHSQNPYTHA/HAADYTOAMCYLKEPKLASFPLTDIMIGL 207
 Database 200 FKLDNVTLHRFLVMQEDYHSQNPYTHA/HAADYTOAMCYLKEPKLASFPLTDIMIGL 259
 Query 208 LAAAHHDVHPGVNQOPPLKTNHHLANLYQMSYLEHNHWSTGMLRSRLLAHLPKEM 267
 Database 260 LAAAHHDVHPGVNQOPPLKTNHHLANLYQMSYLEHNHWSTGMLRSRLLAHLPKEM 319
 Query 268 T 268
 Database 320 T 320

RESULT 8
 Sequence 2, Application US/09602735B
 Patent No. 6656717
 GENERAL INFORMATION:
 APPLICANT: Xin, Xiaonian
 APPLICANT: Unterbeck, Axel
 APPLICANT: Hu, Yingle
 TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
 TITLE OF INVENTION: Use
 FILE REFERENCE: 453260-55
 CURRENT APPLICATION NUMBER: US/09/602,735B
 CURRENT FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: U.S. 60/141,196
 PRIOR FILING DATE: 1999-06-25
 NUMBER OF SEQ ID NOS: 21
 SEQ ID NO 2
 LENGTH: 518
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-602-735B-2

Query Match 25.1%; Score 604.5; DB 2; Length 518;
 Best Local Similarity 33.3%; Pred. No. 8e-55;
 Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Query 66 KKKVKRLLS---PQRYFHDASRLRGIIPOAPLHLLDBDYLGQARHMLSKVGMWDFDIFL 121
 Database 63 KEKCKRPMQSISGVKLMSSSLTNSISREFGVTEQEVDYLAKE--LEDVNKGGLAYER 119
 Query 122 FDRLTNGNSLVTLCH-LFNTHGLIHFMDVTLHRFLVMQDHYHSNPYNAVHAD 180
 Database 120 IABEL-SGNRPLTVIMHTIPOERDLIKTFKIPVDTLITMLEDHYHADVAHNHHA 178
 Query 181 VTOAMHCYLKEPKLASFPLTDIMIGLAAAHVDHPCVNOPLIKTMHHLANLYQMS 240
 Database 179 VVQSTHVLLSTPALEAVFTDLEILAIIFASAIDHVDHPGSNQFLINTNSEALMYNDSS 238
 Query 241 VLENHHWSTGMLRESR--LLAHLPKENTQDIEQQQLGSLLATDINRONEFUTRLKAH 298
 Database 239 VLENHHLAVGFKLUQBNENDCIFONLTKQROSURKMTIVLADLKTVM 298
 Query 299 HNKD----LRLEDAQDRHEFMLQITALKAGIDCNPCTRIVMSKOWSERCEEFYRGDE 352
 Database 299 ETKKVTSGGVLLDNYSRDLQVLMQMVHADLSNPTKPLQYRWTDRIMEFFQGDRE 358
 Query 353 QKFELEISPLCNCQKDSIPISTQIGPMSTYVBPLFREWAHTGNSTLSENMLGHLAHNKAQ 412
 Database 359 RERGMESIPSMCDKHNASVKSQVGPIDYVHPLNETWDLVHPD--AQDILDTLEDNREW 416
 Query 413 WKSLLPRQRHRSRGSSGGPQDHAGQGTSE-----EQEGDS 449
 Database 417 YQSTTPQ-----SPSPAPDDPEEGRQQTEKFQFFLTLEDGES 455
 Query 454 ETRKKVTSSCVLUDNYSRQIQLNQMVHACDLNSNPTKBLQYRWTDRIMEFFQGDRE 513

RESULT 9
 US-08-474-379C-63
 Sequence 63, Application US/08474379C
 Patent No. 5977305
 GENERAL INFORMATION:
 APPLICANT: Wigler, Michael H.
 APPLICANT: Colicelli, John J.
 TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
 TITLE OF INVENTION: PROCESSES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive/6300 Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,379C
 APPLICATION NUMBER: US/08/474,379C
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/206,188
 FILING DATE: 01-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/688,352
 FILING DATE: 19-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 27866/322771
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 INFORMATION FOR SBQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-474-379C-63

Query Match 25.1%; Score 604.5; DB 1; Length 673;
 Best Local Similarity 33.3%; Pred. No. 1.e-54;
 Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;
 Query 66 KKVKRLLS---PQRYFHDASRLRGIIPOAPLHLLDBDYLGQARHMLSKVGMWDFDIFL 121
 Database 275 IAEI-SGRPLTVIMHTIPOERDLIKTFKIPVDTLITMLEDHYHADVAHNHHA 212
 Query 218 KEKCKRPMQSISGVKLMSSSLTNSISREFGVTEQEVDYLAKE--LEDVNKGGLAYER 274
 Database 122 FDRLTNGNSLVTLCH-LFNTHGLIHFMDVTLHRFLVMQDHYHSNPYNAVHAD 180
 Query 275 VVQSTHVLLSTPALEAVFTDLEILAIIFASAIDHVDHPGSNQFLINTNSEALMYNDSS 333
 Database 275 IAEI-SGRPLTVIMHTIPOERDLIKTFKIPVDTLITMLEDHYHADVAHNHHA 333
 Query 181 VTQAMHCYLKEPKLASFPLTDIMIGLAAAHVDHPCVNOPLIKTMHHLANLYQMS 240
 Database 334 VVQSTHVLLSTPALEAVFTDLEILAIIFASAIDHVDHPGSNQFLINTNSEALMYNDSS 393
 Query 241 VLENHHWSTGMLRESR--LLAHLPKENTQDIEQQQLGSLLATDINRONEFUTRLKAH 298
 Database 394 VLENHHLAVGFKLUQBNENDCIFONLTKQROSURKMTIVLADLKTVM 298
 Query 299 HNKD-----LRLEDAQDRHEFMLQITALKAGIDCNPCTRIVMSKOWSERCEEFYRGDE 449
 Database 454 ETRKKVTSSCVLUDNYSRQIQLNQMVHACDLNSNPTKBLQYRWTDRIMEFFQGDRE 513

Qy 353 QKFELEISPLCQNQKDSDPSIPIQIGMSVYVEPLFREWAHTGNSTLSENMLGHIAHNKAQ 412
 Db 514 RERGHEISPMCDKHNASVESSQVGPIDYIWHPLNETWALVHPD-AQDILDTLEDNREW 571

Qy 413 WKSULPROHRSRGSSGSPDHAGQGTSE-----EQEGDS 449
 Db 572 YQSTIPQ-----SPSPADPPEGRQQTEKFOPELTUEDGES 610

RESULT 10
 US-09-146-249A-63
 Sequence 63, Application US/09146249A
 Patent No. 6069240
 GENERAL INFORMATION:
 APPLICANT: Wigler, Michael H.
 APPLICANT: Colicelli, John J.
 TITLE OF INVENTION: Cloning by Complementation and Related
 TITLE OF INVENTION: Processes
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/146,249A
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-6300
 TELEX: 25-3856
 MOLECULE TYPE: protein
 US-09-146-249A-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;
 Best Local Similarity 33.3%; Pred. No. 1.2e-54;
 Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KCKVKRLIS---FQRYFHASRLRLGIIQPAQPHLLDLGOARHMLSKGMWDIFL 121
 Db 218 KEKKRKPRMSQISGVKKLMHSSLTNSSIPRFGYKTEQBDVLAKE--LEDVWKWLHVER 274

Qy 122 FDRATNGNSLVTLLCH-LFNTNGLIHHFKLDMVTLHFRFLVMQEDYHSQNPYTHNAHAAD 180
 Db 275 IAEI-SGNRPLITMHTFQERDLKTFKIPUDLITYLMDHYDAVHNHHAAD 333

Qy 181 VTOAMHCYKLKEPKLASFLPTLDIMLGIIAAAHDVDPHGVNQFLIKTNHHLANLYONMS 240
 Db 334 VVQSTHVLLSTPALEAVTDLLEIAAFASATHDVDFGSNSQFLNTSELAMYNDSS 393

Qy 241 VLENHAWRSTIGMLRESR-LLAHLPKEMTQDIEQLQSLILATDINRQEFLTRIKAH 298
 Db 394 VLENHHLAVGFKLUQEENDIFQNLTKQROSRLRMVTDIVLATDMSKHNLLADLKTMV 453

Qy 299 HNKD-----LRILEDQDRHFMILQIALKCADICNPKRIWEMSOKWSERVICEFFYRQGEL 352
 Db 454 ETKKVTTSCVLLDNYSDRIVQVQNMVFCADSNTPKLQLYRQWTDLIMEFPRQGDRE 513

Qy 353 QKFELEISPLCQNQKDSDPSIPIQIGMSVYVEPLFREWAHTGNSTLSENMLGHIAHNKAQ 412
 Db 514 RERGHEISPMCDKHNASVESSQVGPIDYIWHPLNETWALVHPD-AQDILDTLEDNREW 571

Qy 413 WKSULPROHRSRGSSGSPDHAGQGTSE-----EQEGDS 449
 Db 572 YQSTIPQ-----SPSPADPPEGRQQTEKFOPELTUEDGES 610

RESULT 11
 US-08-206-188B-63
 Sequence 63, Application US/08206188B
 Patent No. 6100025
 GENERAL INFORMATION:
 APPLICANT: Wigler, Michael H.
 APPLICANT: Colicelli, John J.
 TITLE OF INVENTION: Cloning by Complementation and Related
 TITLE OF INVENTION: Processes
 NUMBER OF SEQUENCES: 84
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/206,188B
 FILING DATE: 01-MAR-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 20-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-206-188B-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;
 Best Local Similarity 33.3%; Pred. No. 1.2e-54;
 Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KCKVKRLIS---FQRYFHASRLRLGIIQPAQPHLLDLGOARHMLSKGMWDIFL 121
 Db 218 KEKKRKPRMSQISGVKKLMHSSLTNSSIPRFGYKTEQBDVLAKE--LEDVWKWLHVER 274

Qy 122 FDRATNGNSLVTLLCH-LFNTNGLIHHFKLDMVTLHFRFLVMQEDYHSQNPYTHNAHAAD 180
 Db 275 IAEI-SGNRPLITMHTFQERDLKTFKIPUDLITYLMDHYDAVHNHHAAD 333

Qy 181 VTOAMHCYKLKEPKLASFLPTLDIMLGIIAAAHDVDPHGVNQFLIKTNHHLANLYONMS 240
 Db 334 VVQSTHVLLSTPALEAVTDLLEIAAFASATHDVDFGSNSQFLNTSELAMYNDSS 393

Qy 241 VLENHAWRSTIGMLRESR-LLAHLPKEMTQDIEQLQSLILATDINRQEFLTRIKAH 298
 Db 394 VLENHHLAVGFKLUQEENDIFQNLTKQROSRLRMVTDIVLATDMSKHNLLADLKTMV 453

Qy 299 HNKD-----LRILEDQDRHFMILQIALKCADICNPKRIWEMSOKWSERVICEFFYRQGEL 352
 Db 454 ETKKVTTSCVLLDNYSDRIVQVQNMVFCADSNTPKLQLYRQWTDLIMEFPRQGDRE 513

Qy 353 QKFELEISPLCQNQKDSDPSIPIQIGMSVYVEPLFREWAHTGNSTLSENMLGHIAHNKAQ 412
 Db 514 RERGHEISPMCDKHNASVESSQVGPIDYIWHPLNETWALVHPD-AQDILDTLEDNREW 571

Qy 413 WKSULPROHRSRGSSGSPDHAGQGTSE-----EQEGDS 449
 Db 572 YQSTIPQ-----SPSPADPPEGRQQTEKFOPELTUEDGES 610

241	VLENHWRSTIGMRESR--LILAHLPKEMTQDIEQGQSLLIATIDINRQNBLPLTRKAHL	298
394	VLENHHLAVGFKLQQENCDIFONLTKKQRQSLSRKWIDIVATDMSKHMNLADLKTMV	453
299	HNKD-----LRLEDAODRFHMLQIAALKCADICNCPRIWEMSKOWNSERVICEFYROGELE	352
454	ETRKVTSSCVLLDNYSRDIQVQLQNMVHCADISNPTEPQLYRQWTDRIMEEFFRQGDRE	513
353	QKPELEISPLCNCQKDSPSIQTGFMSSYIPELPRERWAHFGTGNSTLSENMLGLHANKAQ	412
514	RERGMESIPMCDKHNAVEKSQVGFIDIVHPLWETADLYVHPD--AQDILDTLDNREW	571
413	WKSLLPROHRSGSSGSQGDHDIAQGTESE-----EQEGDS	449
572	YQSTIPQ-----SPSPAPDDPBEGRQOTEKFQFELTLEDGES	610
RESULT 12		
	US-09-602-735B-4	
	Sequence 4, Application US/09602735B	
	Patent No. 665617	
	GENERAL INFORMATION:	
	APPLICANT: Xin, Xiaonan	
	APPLICANT: Unterbeck, Axel	
	APPLICANT: Hu, Yinghe	
	TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of	
	FILE REFERENCE: 452260-55	
	CURRENT APPLICATION NUMBER: US/09/602,735B	
	CURRENT FILING DATE: 2000-06-23	
	PRIOR APPLICATION NUMBER: U.S. 60/141,196	
	PRIOR FILING DATE: 1999-06-25	
	NUMBER OF SEQ ID NOS: 21	
	SOFTWARE: Patentin Ver. 2.1	
	SEQ ID NO 4	
	LENGTH: 517	
	TYPE: PRT	
	ORGANISM: Rattus sp.	
	US-09-602-735B-4	
Qy	Query Match Best Local Similarity保守性 Matches 135; Conservative Matches 85; Mismatches 152; Indels 33; Gaps 9;	
Ddb	66 KKEKVRLLS----FORYPHASRLRGITQPALHLLBDYLGQARMLSKVGMWDFDIFL 121 63 KEKCKRPMSQISGVTKLMHSSSLTNSCIPRFGVKTBQEDVLAK--LEDYTKWGLHVFR 119	
Qy	122 FDRLTNGNLSLVTLCH-LFNTNGLHFLKDLNVTLHFLVMQEDYHSQNPYHNAVHAAD 180 120 IAE---SGRPLRTVIMHTI.FQERDLKLTKPVIDLTLYMLTDYHTHADVAYHNNAHAD 178	
Ddb	181 VTQAMHCYIKEPKLASFTPLDIMGLLAAAHDVHPGYNQPELKTMMHHLANLYQNMS 240 179 VVQSTHVLSTPALEAVFTDLEIATAIFASATHDVDPGVSNQFLINTNSBLAUYNDDS 238	
Qy	241 VLENHWRSTIGMRESR--LILAHLPKEMTQDIEQGQSLLIATIDINRQNBLPLTRKAHL	298
Ddb	239 VLENHHLAVGFKLQQENCDIFONLTKKQRQSLSRKWIDIVATDMSKHMNLADLKTMV	453
Qy	299 HNKD-----LRLEDAODRFHMLQIAALKCADICNCPRIWEMSKOWNSERVICEFYROGELE	352
Ddb	299 ETRKVTSQGVLLDNYSRDIQVQLQNMVHCADISNPTEPQLYRQWTDRIMEEFFRQGDRE	513
353	QKPELEISPLCNCQKDSPSIQTGFMSSYIPELPRERWAHFGTGNSTLSENMLGLHANKAQ	412
359	RERGMESIPMCDKHNAVEKSQVGFIDIVHPLWETADLYVHPD--AQDILDTLDNREW	416
413	WKSLLPROHRSGSSGSQGDHDIAQGTESE-----EQEGDS	449
417	YQSTIPQ-----SPSPAPDDPBEGRQOTEKFQFELTLEDGES	455

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RESULT 13
US-08-577-492-35
; Sequence 35 , Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; NUMBER OF SEQUENCES: 40
; CURRENT ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/577,492
FILING DATE: 22-DEC-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: unknown

US-08-577-492-35

Query Match          Score 599.5; DB 54; Length 673;
Best Local Similarity          33.6%; Pred. No. 4.1e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 0

Qy  66 KKKVRLIS---FQRYPHASRLRGLIPQAPHLDDFLGQARHMLSKVGWMDFDIFL
Db  218 KEKCKRPNSQISGVKMHSSLTNSTNSSIPRFGVYTKTEQDVLAKE--LEDVNKGLEYVER
Qy  122 FDRDLTGNSLTVLILCH-LFNTNGLHHFKLDDMTYLHRLPFLVVODYHSONYHNAVHAD
Db  275 IAEI-SGARPLTVYIMHTIFQERDLKTKPFIKVDTLVLMTLEHYHADYAVHNHAID
Qy  181 VPOAMHCYIKEPKLASFTPLDIMGLLAAGAHVDHPGIVNQPLIKTNHHLANYONMS
Db  334 VVQTHVILSTPALEAVFTDLETLAATPASAITHDVDPGVSNQFLINTSELAMYNDSS
Qy  241 VLENHWHRSTIGMRESR--LLAHPLKEMTDLHQQLGSLLILATDINFONBFLTRLKHAL
Db  394 VLENHLLAVGPKLQOBENCDIFQNLTKQRQSLRKMVIDVLATDMSKHMNLLADLKTVM
Qy  299 HNKD-----LRLDEAQDRHFMQLIAALKCADICNPCTRIWEMSOWSERVCEEFYRQGELE
Db  454 ETKKVTS5GVLLDNYSRIVQ1QNMVYCAIDSNPTEQLQLFQWTDIMEBFQQDRE
Qy  353 QKEPELSPLCNOQKDPSIPIQIGMSVIEPLFRENWAHTGNSTLSRMGLHLANKAQ

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514 RERGMETISPMCDKHNASVKEKSVQGFDIYVHPLMETHAALVHPD-AQDILDITLEDNEW 571

513 WKSLLPROHRSRGSSGGPDDHDHAG-OCTESE-----EOEGDS 449

512 YQSTIPQ-----SPSPAPDDPEBGRQQGTGKFOELTIEBEDGES 610

RESULT 14
US-09-079-630-35
Sequence 35, Application US/09079630
Patient No. 6291199
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
APPLICANT: Lumb, Simon Mark
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
TITLE OF INVENTION: ITS PRODUCTION AND USE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199r18
CITY: One Liberty Place, 46th Floor
STATE: PA
ZIP: 19103
CITY: Philadelphia
STATE: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 630
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/577, 492
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TOPOLogy: unknown
US-09-079-630-35

Query Match 24.9%; Score 599.5; DB 2; Length 673;
Best Local Similarity 33.6%; Pred. No. 4.1e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;

66 KKKVKRLLS---FQRYPHASRLLRGIFTQAPIHLILDDYLGQARHMLSKVGNWDFDIFL 121

218 KEKKKRPMQSISGVKLMKMHSSSLTNSSPRFGVKTQEVDVLAKE--LEDVWKGLHVER 274

Query Match 24.1%; Score 580.5; DB 1; Length 562;
Best Local Similarity 31.9%; Pred. No. 3.1e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

66 KKKVKRLLS---FQRYPHASRLRGTIPQAPIHLILDDYLGQARHMLSKVGNWDFDIFL 121

124 KKKKQMLTQISGVKLMHSSSLTNNTSISRFVNTNEDHLAKELDNLK--WGLNIFN 180

Db 275 IAEL-SGRRPLTVIATIFQERULLKTFKIPVDTLTLMTDHYADVAHHNHAAD 333

181 VTOQAMHCYKKEPKLASPLTPLDIMLGLIAAAHDVDPGVNQPELIKNNHLLANLYONMS 240

334 VQSTHVLISTPALEAVFTDLELIAAFASATHDVDFGVSQFLINTNSEALMNDSS 393

241 VLENHHRWSTIGMRESR-LLAHLPKEMTQDIEQQLGSLLATDINRNQNBLTRALKH 298

Db 394 VLENHHLAVGPKLQLQENCIDFONLTKKQRQSURKMMVIDIVLATDMSKHMNLLADLKTIV 453

299 HKND-----LRLBEDAQDRHFMILQLALKCADICNPCCRWMKOWSERVICEEFYRQGELE 352

454 ETRKVTSSCVLLDNYSIRQVLMNMYHACDLNPNTRPLQLXQWTDEIMEBFRQGDRE 513

353 QKFELEISPLCNOQKDSIPISIQGMSVIVEPLFREWAHTFGNSTLSENMLGHLAHNKAQ 412

514 RERGMETISPMCDKHNASVKEKSVQGFDIYVHPLMETHAALVHPD-AQDILDITLEDNEW 571

Qy 413 WKSLLPROHRSRGSSGGPDDHDHAG-OCTESE-----EQEDS 449

Db 572 YQSTIPQ-----SPSPAPDDPEBGRQQGTGKFOELTIEBEDGES 610

RESULT 15
US-07-688-352C-4
Sequence 4, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688, 352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511, 715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELE: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-688-352C-4

Query Match 24.1%; Score 580.5; DB 1; Length 562;
Best Local Similarity 31.9%; Pred. No. 3.1e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

Qy 66 KKKVKRLLS---FQRYPHASRLRGTIPQAPIHLILDDYLGQARHMLSKVGNWDFDIFL 121

Db 124 KKKKQMLTQISGVKLMHSSSLTNNTSISRFVNTNEDHLAKELDNLK--WGLNIFN 180

122 FDRITNGSLVLLCH-LFNTNTHGKFLDWYQDYSQHNPYNAHAAD 180

Qy 181 VTOQAMHCYKKEPKLASPLTPLDIMLGLIAAAHDVDPGVNQPELIKNNHLLANLYONMS 240

Db 334 VQSTHVLISTPALEAVFTDLELIAAFASATHDVDFGVSQFLINTNSEALMNDSS 393

Qy 241 VLENHHRWSTIGMRESR-LLAHLPKEMTQDIEQQLGSLLATDINRNQNBLTRALKH 298

Db 181 VAGYSNRPLTCIMAYAFOERDLLKTFKISSDTFVYMMTLEDYHSDVAYNSLRAADV 240

182 TQAMHCYLKEPKLASFLTPLDIMLGILAAAHDYDHPGYNQPELJKTNEHHLANLYQNM SY 241
 241 :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
 Db AOSTHVLLSPALDAFTDIBILAAIFAAIAHVDHPGSNOFLINTNEBALMYNDEV 300
 Qy 242 LENHHWRSTIGMLRSR--LLAHLPKEMTODIEQOLGSLLATIDINRQEFLTRLKAHH 299
 301 LENHHLAGFPLQBEHCDIFQNLTKKORQLRMVYDMLVADMSKHNLLADLKTWVB 360
 Qy 300 NKD-----IRLEDQDRHMLQITALKCADIICNPRIENSKOWSERVEFYRGELIQ 353
 Db 361 TKRVTSVGLLNDNTDRIQYLRAVMHCADLSNPTKSLELYRQWTDRINEFFFOGDKER 420
 Qy 354 KFELRISPLCNCQKDPSIPIQIGMSYVBPFLREWAHTFGNSTLSENNMIGHLAHNKAQW 413
 Db 421 ERGMITSPMCIDKHTASVRSQVGFIDYIVHPLWETWADIVQPD--AQDLDTLEDNRNWY 478
 Qy 414 KSLLPR----QHRSRGSSGGPDDHDH---AGGOTSEBEEQEGDSP 450
 479 QSMIFQSPSPPLDERSRDQGLMEKFQFELTLEBEDSEGPEKECEGP 525

Search completed: March 10, 2006, 20:04:14
 Job time : 41.8537 secs

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OM protein - protein search, using sw model

Run on: March 10, 2006, 20:18:07 ; Search time 135.976 Seconds

(without alignments), 1382.771 Million cell updates/sec

Title: US-10-781-181-5

Perfect score: 2408

Sequence: 1 MSCLMVERCGBILPENPDQN PDHDHAGQTESEQEGDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 45 summaries

Database : Published Applications AA_Main:*

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2: /cn2_6/podata/1/pubpaas/us08_pubcomb.pep:*

3: /cg2_6/podata/1/pubpaas/us09_pubcomb.pep:*

4: /cgn2_6/podata/1/pubpaas/us10_pubcomb.pep:*

5: /cn2_6/podata/1/pubpaas/us10b_pubcomb.pep:*

6: /cg2_6/podata/1/pubpaas/us11_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	100.0	450	4 US-10-781-181-5	Sequence 5, Appli
2	2408	100.0	450	5 US-10-204-268A-2	Sequence 2, Appli
3	2258	93.8	502	4 US-10-273-517-1	Sequence 1, Appli
4	2258	93.8	502	4 US-10-386-414-4	Sequence 4, Appli
5	2258	93.8	502	4 US-10-311-104-1	Sequence 1, Appli
6	2258	93.8	502	6 US-11-048-744-1	Sequence 1, Appli
7	2258	93.8	502	6 US-11-048-744-1	Sequence 1, Appli
8	2192	91.0	446	4 US-10-781-181-1	Sequence 1, Appli
9	1865	77.5	391	5 US-10-204-268A-4	Sequence 4, Appli
10	1801	74.8	335	5 US-10-771-833-23	Sequence 23, Appli
11	1801	74.8	335	5 US-10-886-949-23	Sequence 23, Appli
12	1430	59.4	288	4 US-10-781-181-3	Sequence 3, Appli
13	1410	58.6	426	3 US-09-966-781A-2	Sequence 2, Appli
14	1403	58.3	426	3 US-09-966-781A-1	Sequence 1, Appli
15	1397	58.0	426	3 US-09-966-781A-3	Sequence 4, Appli
16	1287	53.4	424	5 US-10-380-437-6	Sequence 6, Appli
17	1287	53.4	424	5 US-10-380-437-53	Sequence 53, Appli
18	1286	53.4	432	3 US-09-164-989-208	Sequence 208, Appli
19	1280	53.2	320	4 US-10-386-414-6	Sequence 6, Appli
20	1234	51.3	334	5 US-10-771-833-22	Sequence 22, Appli
21	1287	51.3	334	5 US-10-886-949-22	Sequence 22, Appli
22	1194	51.5	336	4 US-10-258-746-2	Sequence 2, Appli
23	771	32.0	211	3 US-09-764-989-280	Sequence 280, Appli
24	771	32.0	211	3 US-09-989-442-120	Sequence 120, Appli
25	604.5	25.1	507	4 US-10-076-597-49	Sequence 49, Appli
26	604.5	25.1	507	4 US-10-067-514-10	Sequence 10, Appli
27	604.5	25.1	507	4 US-10-419-723-10	Sequence 10, Appli

ALIGNMENTS

28	604.5	25.1	507	4 US-10-255-120-10
29	604.5	25.1	507	5 US-10-755-889-304
30	604.5	25.1	518	4 US-10-868-397-10
31	604.5	25.1	585	4 US-10-067-514-9
32	604.5	25.1	585	4 US-10-419-723-9
33	604.5	25.1	585	4 US-10-55-10-9
34	604.5	25.1	585	5 US-10-868-397-9
35	604.5	25.1	664	5 US-10-735-973-2
36	604.5	25.1	673	4 US-10-076-597-51
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41	604.5	25.1	673	5 US-10-735-973-1
42	604.5	25.1	673	5 US-10-067-514-8
43	604.5	25.1	679	5 US-10-735-973-6
44	604.5	25.1	679	5 US-10-067-514-8
45	604.5	25.1	687	4 US-10-067-514-8

RESULT 1					
US-10-781-181-5					
; Sequence 5, Application US/10781181					
; Publication No. US20040137508A1					
; GENERAL INFORMATION:					
; APPLICANT: Pfizer Inc.					
; Fidock, Mark David					
; Enzyme PDE xiv					
; FILE REFERENCE: PC10315B					
; CURRENT APPLICATION NUMBER: US/10/781,181					
; CURRENT FILING DATE: 2004-02-18					
; PRIOR APPLICATION NUMBER: GB 9828603.2					
; PRIOR FILING DATE: 1998-12-23					
; PRIOR APPLICATION NUMBER: US 09/471,459					
; PRIOR FILING DATE: 1999-12-22					
; PRIOR FILING DATE: 1999-09-17					
; NUMBER OF SEQ ID NOS: 26					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO: 5					
; TYPE: PRT					
; ORGANISM: Human					
US-10-781-181-5					
Query Match					
Best Local Similarity					
Matches 450; Conservative 0;					
; Mismatches 0; Indels 0; Gaps 0;					
; 1 MSC1MVERGEILLFENPDONAKCVCMLGDIRLQRGTYRAERGSYPFDIFRLINSTYS 60					
; 1 MSC1MVERGEILLFENPDONAKCVCMLGDIRLQRGTYRAERGSYPFDIFRLINSTYS 60					
; 61 GETGKCKVKRLLSFQRYPHASRLGLRGLIOPAHLDEDYLGQARHMLSKVGMWDFDF 120					
; 61 GEITGKCKVKRLLSFQRYPHASRLGLRGLIOPAHLDEDYLGQARHMLSKVGMWDFDF 120					
; 121 LFDRLTNGLSVLTLCHLPLNTGHGLIHHFKLDMTLHRFLYVMQEDYHSQNYPYNAHAAD 180					
; 121 LFDRLTNGLSVLTLCHLPLNTGHGLIHHFKLDMTLHRFLYVMQEDYHSQNYPYNAHAAD 180					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					
; 121 VTOAMHCYLTKEPKLASFLTPLDMLGLIAAAHDVHPGVNOPLFLKTMNHHLANLYQNM 240					

Db	301	KDLRLEDADQRHFMQLALKCADICNPCTWEMQSOWSERVCBEEYRGLEQKFELIS	360
Qy	361	PLCNQKQDSIPTSIQGMSYIVPEFREWAHTGNSTLSENMLGHLAHNKAQWKSLLPRQ	420
Db	361	PLCNQKQDSIPTSIQGMSYIVPEFREWAHTGNSTLSENMLGHLAHNKAQWKSLLPRQ	420
Qy	421	HRSRGSSGSPDPDHAGQGTSEEBQGDSP	450
Db	421	HRSRGSSGSPDPDHAGQGTSEEBQGDSP	450
Qy	421	HRSRGSSGSPDPDHAGQGTSEEBQGDSP	450
RESULT 2			
US-10-204-268A-2			
; Sequence 2, Application US/10204268A			
; Publication No. US20050058647A1			
; GENERAL INFORMATION:			
; APPLICANT: KLUXEN, FRANZ-WERNER			
; HENTTSCH, BERND			
; TITLE OF INVENTION: PHOSPHODIESTERASE TYPE 7B			
; FILE REFERENCE: MERCK-248A ⁴			
; CURRENT APPLICATION NUMBER: US/10/204,268A			
; CURRENT FILING DATE: 2004-08-20			
; PRIOR APPLICATION NUMBER: PCT/EP01/01858			
; PRIOR FILING DATE: 2002-02-20			
; PRIOR APPLICATION NUMBER: EP 00103655.7			
; PRIOR FILING DATE: 2000-02-21			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO: 2			
; LENGTH: 450			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-204-268A-2			
Query Match	100.0%	Score 2408; DB 5; Length 450;	
Best Local Similarity	100.0%	Pred. No. 9 2e-226;	
Matches	450;	Mismatches 0;	
		Indels 0;	
		Gaps 0;	
Qy	1	MSCLMVERGEELLPEPNPDONAKCVCMLGDI1RLRCGTGVAERRSSYPFDERLUNISTRYS	60
Db	1	MSCLMVERGEELLPEPNPDONAKCVCMLGDI1RLRCGTGVAERRSSYPFDERLUNISTRYS	60
Qy	61	GEI GTKKVYKRLLSFRQYFHASRLRGIIQPAQPHLDEDYLQGARHMLSKVGWMDFDIF	120
Qy	61	GEI GTKKVYKRLLSFRQYFHASRLRGIIQPAQPHLDEDYLQGARHMLSKVGWMDFDIF	120
Db	121	L PBLTNGNSLVLTLCHLPLNTHGLIHFKLDMYTILHRFLYMQDSDYHSONPYNAVHAAD	180
Db	121	L PBLTNGNSLVLTLCHLPLNTHGLIHFKLDMYTILHRFLYMQDSDYHSONPYNAVHAAD	180
Qy	181	VTOAMHCYLIKEPKLASFITPLDIMGLLAAAHDVDHPGVNQOPFLIKTNHHLANLYQNMS	240
Db	181	VTOAMHCYLIKEPKLASFITPLDIMGLLAAAHDVDHPGVNQOPFLIKTNHHLANLYQNMS	240
Qy	241	VLENHHWSTIGMLRESRLAHLPKEMTDIEQQLSLLATDINRONEFLTRLKAHLHN	300
Db	241	VLENHHWSTIGMLRESRLAHLPKEMTDIEQQLSLLATDINRONEFLTRLKAHLHN	300
Qy	301	KDLRLEDADQRHFMQLALKCADICNPCTWEMQSOWSERVCBEEYRGLEQKFELIS	360
Db	301	KDLRLEDADQRHFMQLALKCADICNPCTWEMQSOWSERVCBEEYRGLEQKFELIS	360
Qy	361	PLCNQKQDSIPTSIQGMSYIVPEFREWAHTGNSTLSENMLGHLAHNKAQWKSLLPRQ	420
Db	361	PLCNQKQDSIPTSIQGMSYIVPEFREWAHTGNSTLSENMLGHLAHNKAQWKSLLPRQ	420
Qy	421	HRSRGSSGSPDPDHAGQGTESBQGDSP	450

RESULT 4
US-10-386-414-4
i. Semence A. Application US/10386414

Publication No. US20040006016A1
 GENERAL INFORMATION:
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Robison, Keith E.
 APPLICANT: White, David
 APPLICANT: Williamson, Mark W.
 APPLICANT: Cook, William James
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Macbeth, Kyle J.
 APPLICANT: Carroll, Joseph M.
 APPLICANT: Chun, Mi-Young
 TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
 TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
 FILE REFERENCE: MPI03-0210NM
 CURRENT APPLICATION NUMBER: US10/386,414
 CURRENT FILING DATE: 2003-03-11
 PRIOR APPLICATION NUMBER: 09/426,282
 PRIOR FILING DATE: 1999-10-25
 PRIOR APPLICATION NUMBER: 09/568,266
 PRIOR FILING DATE: 2000-09-22
 PRIOR APPLICATION NUMBER: 09/330,970
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: 09/724,599
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 09/860,193
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 10/283,023
 PRIOR FILING DATE: 2002-10-29
 PRIOR APPLICATION NUMBER: 60/335,044
 PRIOR FILING DATE: 2001-10-31
 PRIOR APPLICATION NUMBER: 10/010,943
 PRIOR FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: 60/254,037
 PRIOR FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: 09/333,082
 PRIOR FILING DATE: 2001-04-10
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-386-414-4

Query Match 93.8%; Score 2258; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 4.7e-21; Mismatches 0; Indels 0; Gaps 0;
 Matches 423; Conservative 0; Gaps 0;

Qy 28 GDIRLRGQTGVRARERGSPFDIPLLNSTYSGBIGTKKKVRLLSFORYFHASRLRG 87
 Db 80 GDIRLRGQTGVRARERGSPFDIPLLNSTYSGBIGTKKKVRLLSFORYFHASRLRG 139

Qy 88 IIPOAPLHIDEDYLQARHMLSKVGMWDFDIFFDRLTNGNSLVTLCHLFNTHGLIH 147
 Db 140 IIPOAPLHIDEDYLQARHMLSKVGMWDFDIFFDRLTNGNSLVTLCHLFNTHGLIH 199

Qy 148 FKLDMVTLHREFLVWQEDTHSONPYHNAADTVQAMHCYLKEPKLASFLTPLDIMGGL 207
 Db 200 FKLDMVTLHREFLVWQEDTHSONPYHNAADTVQAMHCYLKEPKLASFLTPLDIMGGL 259

Qy 208 LAAAHHDVDFHPGVNQPLIKTNHHLANLYQNMSLENHWRSTIGMLRSRLLAHLPKEM 267
 Db 260 LAAAHHDVDFHPGVNQPLIKTNHHLANLYQNMSLENHWRSTIGMLRSRLLAHLPKEM 319

Qy 268 TQDIEQQLSLILATDINRNEFLTRKALHNKDLRLEDQDRHFMQLQIALKCADICNP 327
 Db 320 TQDIEQQLSLILATDINRNEFLTRKALHNKDLRLEDQDRHFMQLQIALKCADICNP 379

Qy 328 CRIWMSKQNSERVICEEFVQGELBQKFELISPLCNOQDKSDPSIQGMSVTEPLFR 387
 Db 380 CRIWMSKQNSERVICEEFVQGELBQKFELISPLCNOQDKSDPSIQGMSVTEPLFR 439
 Qy 388 EWAHTGNSTLSENLMLGHNAOKWSLPRHRSRGSSGSPDHAGQGTSEEQEG 447

Db 440 EWAHTGNSTLSENLMLGHNAOKWSLPRHRSRGSSGSPDHAGQGTSEEQEG 499

RESULT 5
 US-10-311-104-1 ; Sequence 1, Application US/10311104
 Publication No. US200400054138A1
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: THORNTON, Michael
 APPLICANT: DING, Li
 APPLICANT: ARIVUZU Chandra S.
 APPLICANT: YAO, Monique G.
 APPLICANT: TRIBOURLY, Catherine M.
 APPLICANT: LAL, Preeti G.
 APPLICANT: HAFLIA, April J. A.
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: RAMKUMAR, Jayalaxmi
 APPLICANT: LU, Yan
 APPLICANT: CHAWLA, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 PCT
 CURRENT APPLICATION NUMBER: US/10/311,104
 CURRENT FILING DATE: 2002-12-12
 PRIOR APPLICATION NUMBER: PCT/US01/20140
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/213,741
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 60/218,234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/241,100
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PERL program
 SEQ ID NO 1
 LENGTH: 502
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
 US-10-311-104-1

Query Match 93.8%; Score 2258; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 4.7e-21; Mismatches 0; Indels 0; Gaps 0;
 Matches 423; Conservative 0; Gaps 0;

Qy 28 GDIRLRGQTGVRARERGSPFDIPLLNSTYSGBIGTKKKVRLLSFORYFHASRLRG 87
 Db 80 GDIRLRGQTGVRARERGSPFDIPLLNSTYSGBIGTKKKVRLLSFORYFHASRLRG 139

Qy 88 IIPOAPLHIDEDYLQARHMLSKVGMWDFDIFFDRLTNGNSLVTLCHLFNTHGLIH 147
 Db 140 IIPOAPLHIDEDYLQARHMLSKVGMWDFDIFFDRLTNGNSLVTLCHLFNTHGLIH 199

Qy 148 FKLDMVTLHREFLVWQEDTHSONPYHNAADTVQAMHCYLKEPKLASFLTPLDIMGGL 207
 Db 200 FKLDMVTLHREFLVWQEDTHSONPYHNAADTVQAMHCYLKEPKLASFLTPLDIMGGL 259

Qy 208 LAAAHHDVDFHPGVNQPLIKTNHHLANLYQNMSLENHWRSTIGMLRSRLLAHLPKEM 267
 Db 260 LAAAHHDVDFHPGVNQPLIKTNHHLANLYQNMSLENHWRSTIGMLRSRLLAHLPKEM 319

Qy 268 TQDIEQQLSLILATDINRNEFLTRKALHNKDLRLEDQDRHFMQLQIALKCADICNP 327
 Db 320 TQDIEQQLSLILATDINRNEFLTRKALHNKDLRLEDQDRHFMQLQIALKCADICNP 379

Qy 328 CRIWMSKQNSERVICEEFVQGELBQKFELISPLCNOQDKSDPSIQGMSVTEPLFR 387
 Db 380 CRIWMSKQNSERVICEEFVQGELBQKFELISPLCNOQDKSDPSIQGMSVTEPLFR 439
 Qy 388 EWAHTGNSTLSENLMLGHNAOKWSLPRHRSRGSSGSPDHAGQGTSEEQEG 447

Qy 388 EWAHTGNSTLSENMIGHLAHNKAQWKSLLPROHRSRGSSGSPDHAGQGTSEEQBG 447
 Db 440 EWAHTGNSTLSENMIGHLAHNKAQWKSLLPROHRSRGSSGSPDHAGQGTSEEQBG 499

Qy 448 DSP 450
 Db 500 DSP 502

RESULT 8

US-10-781-181-1
 i Sequence 1, Application US/10781181
 i Publication No. US20040137508A1

i GENERAL INFORMATION:
 i APPLICANT: Pfizer Inc.
 i FILE REFERENCE: PC10315B

i CURRENT APPLICATION NUMBER: US/10/781,181
 i CURRENT FILING DATE: 2004-02-18
 i PRIORITY NUMBER: GB 9328603.2
 i PRIOR FILING DATE: 1998-12-23
 i PRIORITY NUMBER: US 09/471,459
 i PRIOR FILING DATE: 1999-12-22
 i PRIORITY NUMBER: GB 9922123.6
 i PRIOR FILING DATE: 1999-09-17
 i SOFTWARE: PatentIn version 3.2
 i SEQ ID NO: 1
 i LENGTH: 446
 i TYPE: PRT
 i ORGANISM: Mouse

US-10-781-181-1

Query Match 91.0%; Score 2192; DB 4; Length 446;
 Best Local Similarity 91.6%; Pred. No. 1.1e-204;
 Matches 413; Conservative 13; Indels 6; Gaps 2;

Qy 1 MSCLMVERCGSFLNPQDQAKCYCNGLDRLRGTGVAAERRSYPPFDERLNNTSY 60
 Db 1 MSCLMVERCGSFLNPQDQAKCYCNGLDRLRGTGVAAERRSYPPFDERLNNTSY 60

Qy 61 GEIGTKKKYKRLLSFORYFASRLURGLIPOAQLHLDDEYLQARHMLSKVGMWDFFDIF 120
 Db 61 GEIGTKKKYKRLLSFORYFASRLURGLIPOAQLHLDDEYLQARHMLSKVGMWDFFDIF 120

Qy 121 LFDRLTNGSLVTLYLCHLFNTHGLIHKPLDMTILHRLPQYDHSQNPYNAVAHD 180
 Db 121 LFDRLTNGSLVTLYLCHLFNTHGLIHKPLDMTILHRLPQYDHSQNPYNAVAHD 180

Qy 181 VTOAMHCYKLKEPKLASFLPDLIGLAAAHDYDHPGYNQPFLLKTMHLANLYQNS 240
 Db 181 VTQAMHCYKLKEPKLASFLPDLIGLAAAHDYDHPGYNQPFLLKTMHLANLYQNS 240

Qy 241 VLENTHWRSTGMRRESRLIAHLPLKEMTQDIEQOLGSLLATDINRNQBLTRIKAHLIN 300
 Db 241 VLENTHWRSTGMRRESRLIAHLPLKEMTQDIEQOLGSLLATDINRNQBLTRIKAHLIN 300

Qy 361 PLCNOQKDSIPS1QIGFMSTIVEPLREWAHTGNSTLSNNMLGHLAHNKAQWKSLLPQ 420
 Db 361 PLCNOQKDSIPS1QIGFMSTIVEPLREWAHTGNSTLSNNMLSHLARKNAQWKSLLSNQ 420

Qy 421 HRSRGSSGSPDHAGQGTSEEQ-BGDSP 450
 Db 421 HRRRGSG-----QDLGAPAPTELGEGATP 446

RESULT 9

US-10-204-268A-4
 i Sequence 4, Application US/10204268A
 i Publication No. US20050058647A1
 i GENERAL INFORMATION:
 i APPLICANT: KLUXEN, FRANZ-WERNER
 i FILE REFERENCE: MERCK-2484
 i CURRENT APPLICATION NUMBER: US/10/204,268A
 i CURRENT FILING DATE: 2002-08-20
 i PRIORITY NUMBER: PCT/EP01/01858
 i PRIOR FILING DATE: 2002-02-20
 i PRIORITY NUMBER: EP 00103655.7
 i PRIOR FILING DATE: 2000-02-21
 i NUMBER OF SEQ ID NOS: 4
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 4
 i LENGTH: 391
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i FEATURE:
 i NAME/KEY: MOD RES
 i LOCATION: (188)
 i OTHER INFORMATION: Pro or His
 i FEATURE:
 i NAME/KEY: MOD RES
 i LOCATION: (387)
 i OTHER INFORMATION: Val, Ala, Asp, Glu or Gly
 US-10-204-268A-4

Query Match 77.5%; Score 1865; DB 5; Length 391;
 Best Local Similarity 92.7%; Pred. No. 7.4e-173;
 Matches 354; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

Qy 52 RLJNSTTYSGEIGTKKKYKRLLSFORYFASRLURGLIPOAQLHLDDEYLQARHMLSK 111
 Db 10 RLJNSTTYSGEIGTKKKYKRLLSFORYFASRLURGLIPOAQLHLDDEYLQARHMLSK 69

Qy 112 VGMMDPDLFEDLTNGSLVTLYLCHLFNTHGLIHKPLDMTILHRLPQYDHSQNP 171
 Db 70 VGMMDPDLFEDLTNGSLVTLYLCHLFNTHGLIHKPLDMTILHRLPQYDHSQNP 129

Qy 172 YHNAVHAADVTQAMHCYKLKEPKLASFLPDLIGLAAAHDYDHPGYNQPFLLKTNH 231
 Db 130 YHNAVHAADVTQAMHCYKLKEPKLASFLPDLIGLAAAHDYDHPGYNQPFLLKTNH 189

Qy 232 LANIYQMSVLENHWRSTGMRRESRLIAHLPLKEMTQDIEQOLGSLLATDINRNQNEFL 291
 Db 190 LANIYQMSVLENHWRSTGMRRESRLIAHLPLKEMTQDIEQOLGSLLATDINRNQNEFL 249

Qy 292 TRLKHLANKDLEDAQDRHEMLQIAALKCADICNPCTIWMSKQWSERVICEFPRQEL 351
 Db 250 TRLKHLANKDLEDAQDRHEMLQIAALKCADICNPCTIWMSKQWSERVICEFPRQEL 309

Qy 352 EQKPELEISPLCNCQKDPS1QIGFMSTIVEPLREWAHTGNSTLSNNMLGHLAHNKA 411
 Db 310 EQKPELEISPLCNCQKDPS1QIGFMSTIVEPLGAHFTGNSNLQRTCWATFAHNG 369

Qy 412 QWKSLLPRQRHRSRGSSGSPDH 433
 Db 370 QWKSLLPSSTEAGALAXGLDH 391

RESULT 10
 US-10-771-833-23
 i Sequence 23, Application US/10771833
 i Publication No. US2005008573A1
 i GENERAL INFORMATION:
 i APPLICANT: MILBURN, MICHAEL V.
 i FILE REFERENCE: 039163-1106
 i CURRENT APPLICATION NUMBER: US/10/771,833
 i CURRENT FILING DATE: 2004-02-03

PRIOR APPLICATION NUMBER: 60/485, 627
 PRIOR FILING DATE: 2003-07-07
 PRIOR APPLICATION NUMBER: 60/444, 734
 PRIOR FILING DATE: 2003-02-03
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO: 23
 LENGTH: 335
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-771-833-23

Query Match 74.8%; Score 1801; DB 5; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1e-166;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GIIPQAPLHILDEDYLQRHMLSKVGMWDFDIEFLDRITNGSLVTLLCHLFNTGLIH 146
 Db 1 GIIPQAPLHILDEDYLQRHMLSKVGMWDFDIEFLDRITNGSLVTLLCHLFNTGLIH 60

Qy 147 HFKLDMDVTLHRFLYMWQEDYHSQNPAHVAADTVQAHCYLKEPKLASFLTPLDMIG 206
 Db 61 HFKLDMDVTLHRFLYMWQEDYHSQNPAHVAADTVQAHCYLKEPKLASFLTPLDMIG 120

Qy 207 LLAAAABHDYDHPGYNQPFLIKTNHLANLYQNSVLHENHWRSTIGMRLRESRLAHLPKB 266
 Db 121 LLAAAABHDYDHPGYNQPFLIKTNHLANLYQNSVLHENHWRSTIGMRLRESRLAHLPKB 180

Qy 267 MTQDIEQQGSLILATDINRNEFLTRLKAHLHKDLRLEDQDRHMLQIAULKCADICN 326
 Db 181 MTQDIEQQGSLILATDINRNEFLTRLKAHLHKDLRLEDQDRHMLQIAULKCADICN 240

Qy 327 PCRIWEMSKOWSERVCEEFYRGEELEQKPELEISPLCNQKDSIPTQJGMSYIVEPLF 386
 Db 241 PCRIWEMSKOWSERVCEEFYRGEELEQKPELEISPLCNQKDSIPTQJGMSYIVEPLF 300

Qy 387 REWAHTGTNSTLSBNMGLHLANKQWSLLPRQH 421
 Db 301 REWAHTGTNSTLSBNMGLHLANKQWSLLPRQH 335

RESULT 12
 US-10-781-181-3

Qy Sequence 3, Application US/10781181
 Db Publication No. US20040137508A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; Fidock, Mark David
 ; TITLE OF INVENTION: Enzyme PDE xiv
 ; FILE REFERENCE: PC10315B
 ; CURRENT APPLICATION NUMBER: US/10/781,181
 ; CURRENT FILING DATE: 2004-02-18
 ; PRIOR APPLICATION NUMBER: GB 9828603 .2
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/471,459
 ; PRIOR FILING DATE: 1999-12-22
 ; PRIOR APPLICATION NUMBER: GB 9922123 .6
 ; PRIOR FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 3
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-781-181-3

Query Match 59.4%; Score 1430; DB 4; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.e-130;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENFDQNAKCVCMGDIRARGOTCVRAERGSFIDFRLNLNTTYS 60
 Db 1 MSCLMVERCGEILFENFDQNAKCVCMGDIRARGOTCVRAERGSFIDFRLNLNTTYS 60

Qy 61 GE GTKKVKRLLSFQYFHASRLLRGTIPQAPLHILDEDYLQARIMLSKVGMWDIF 120
 Db 61 GE GTKKVKRLLSFQYFHASRLLRGTIPQAPLHILDEDYLQARIMLSKVGMWDIF 120

Qy 121 LPDRLTNGSLVTLCHLFNTGLIHFFKLDMVTLHRFLVMQEDTHSQNPYTHNAHAD 180
 Db 121 LPDRLTNGSLVTLCHLFNTGLIHFFKLDMVTLHRFLVMQEDTHSQNPYTHNAHAD 180

Qy 181 VTOAMHCYLKPEKLASFLTPLDMIGLAAAHVDHPGVNOFLKTNHHLANLYONMS 240
 Db 181 VTOAMHCYLKPEKLASFLTPLDMIGLAAAHVDHPGVNOFLKTNHHLANLYONMS 240

Qy 241 VLENHHRSTIGMRLRESRLAHLPKMT 266
 Db 241 VLENHHRSTIGMRLRESRLAHLPKMT 266

RESULT 13

Query Match 74.8%; Score 1801; DB 5; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1e-166;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GIIPQAPLHILDEDYLQRHMLSKVGMWDFDIEFLDRITNGSLVTLLCHLFNTGLIH 146
 Db 1 GIIPQAPLHILDEDYLQRHMLSKVGMWDFDIEFLDRITNGSLVTLLCHLFNTGLIH 60

US-09-966-781A-2
; Sequence 2, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; CURRENT APPLICATION NUMBER: A0000281US
; FILE REFERENCE: A0000281US
; CURRENT FILING DATE: 2001-09-28
; PRIORITY APPLICATION NUMBER: EP004026637
; NUMBER OF SEQ ID NOS: 35
; PRIORITY FILING DATE: 2000-09-28
; SEQ ID NO: 2
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-966-781A-2

	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Gaps
Qy	18 DQNAKCVCVMGDIRIRGOTVRAERGSRPFDIFFLNNSSTYSGFIGTRKKVKRLLSQR	1410.5;	3	426;	63.1%;	1.9e-128;	1;	1;
Db	1 DQTALEYIRMIGDVRVSRRAGFETTERGSHPYIDFFKHSODIESAVSARNIRLLSQR				67;	Mismatches	84;	Indels
Qy	78 YFHASRLRLRGILIPQAQLHLDDEDYLQGALEMILSKVGMWDFDIELPFDRLTNGNSLVTLCH	137						
Db	61 YLRSLRSPFGATVSSLDLDEDYNGQACRQMLKEQGNWWNDIPLFDRLTNGNSLVSLTFH							
Qy	138 LENTHLGLIHFKLDMVTLHRFLWVQEDYHDSQNPNTHAHAADTVQAMHCYLKEPKLASF	197						
Db	121 LFSLHGLJBFHLMVKLERFLWVQEDYHDSQNPNTHAHAADTVQAMHCYLKEPKLASS							
Qy	198 LTPDLMIGLLAAAHADVPDGPVNQPFLLKTNHHLANLYONMSVLENHWRSTIGMLRES	257.						
Db	181 VTPWDILLSLIARATHDLHPGVNQPFLLKTNHHLATLYKNSSVLENHWRSAVGLLRES							
Qy	258 RLLAHLHPKEMTQDIEQQGSLLIATDINRNEFLTRKAHLHNKDLRLEDAQDRHEFLQI	317						
Db	241 GLFHPHPLRSQNEAQIGALILATDISRNEYLLFRSLDKGDLHLDGGRHRLVLQM							
Qy	318 ALKCADICNPCTWEMSKOMSERVCEEFYQGQELEQKFELISPCPNQQKDSIPIQIGF	377						
Db	301 ALKCADICNPCTWEMPSKQWSBKTYEEFPQGDIEKCYHIGVSPLCDROTESIANIQIGF							
Qy	378 MSYTVEPLPREWAHTFGNTLSENNLGHIAHNKAQWSLLPRQHRSRGSGS	4.29						
Db	361 MTYLVEPLFEWARPSA-TRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAA	4.11						

RESULT 14
US-09-966-781A-1
; Sequence 1, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; CURRENT APPLICATION NUMBER: A0000281US
; FILE REFERENCE: A0000281US
; CURRENT FILING DATE: 2001-09-28
; PRIORITY APPLICATION NUMBER: EP004026637
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-966-781A-1

Db 181 VTPWDILLSLIAATHDLDHPGVNQPFLLIKTNHYLATLXKNTSVLENHWRSAVGLLRES 240
Qy 258 RLLAHLPLKEMTODIEQQGSLILATDINRONEFLTRLK AHLHNKDRLFADADRHEMIGI 317
Db 241 GLFSMLPLESRHEMEAQIGALILATDISQNEYISLFRSHLDKCDLHLDGRHRHLVLOM 300
Qy 318 ALKCADICPCKRINEMSKQNSERVICEEFYRQGELEOKPEFEISPLCNQKDSIPTIQGF 377
Db 301 ALKCADICPCKRANVELSKQWSKSEKTYTEEFPHQGDIEKKYHVGSPLCIDRATESANIQGF 360
Db 378 MSYIVBPLPREWAHTGNSTLSENMLGHIAHNKAQWKSILPROHRSRSSGS 429
Qy 361 MTYLOQBPLFTEWARES-DPLSQTMGLHGVLNKASWKGLQRQQPSSEDASAA 411

Search completed: March 10, 2006, 20:22:34
Job time : 136.976 secs

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OM protein - protein search, using sw mode.

Run on: March 10, 2006, 20:19:01 ; Search time 17.6829 Seconds
 (without alignments)

708.350 Million cell updates/sec

Title: US-10-781-181-5

Pearfect score: 4508

Sequence: 1 MSCUAVERCGBILFFBNPDQN.....PDHDAGQGTSEEEQEGDSP

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 2784885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:
 1: /cgcn2_6/podata/2/pubpaa/us08_new_pub_pep:
 2: /cgcn2_6/podata/2/pubpaa/us06_new_pub_pep:
 3: /cgcn2_6/podata/2/pubpaa/us07_new_pub_pep:
 4: /cgcn2_6/podata/2/pubpaa/pct_new_pub_pep:
 5: /cgcn2_6/podata/2/pubpaa/us05_new_pub_pep:
 6: /cgcn2_6/podata/2/pubpaa/us10_new_pub_pep:
 7: /cgcn2_6/podata/2/pubpaa/us11_new_pub_pep:
 8: /cgcn2_6/podata/2/pubpaa/us00_new_pub_pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	93.8	502	7	US-11-226-701-4	Sequence 4, Appli		
2	1280	53.2	320	7	US-11-226-701-6	Sequence 6, Appli	
3	604.5	25.1	507	7	US-11-091-018-10	Sequence 10, Appli	
4	604.5	25.1	585	7	US-11-091-018-9	Sequence 9, Appli	
5	604.5	25.1	673	7	US-11-091-018-6	Sequence 6, Appli	
6	604.5	25.1	687	7	US-11-091-018-8	Sequence 8, Appli	
7	604.5	25.1	745	7	US-11-091-018-4	Sequence 4, Appli	
8	604.5	25.1	748	6	US-10-492-835-12	Sequence 12, Appli	
9	604.5	25.1	748	6	US-10-492-835-28	Sequence 28, Appli	
10	604.5	25.1	809	7	US-11-091-018-2	Sequence 2, Appli	
11	603.5	25.1	747	6	US-10-492-835-8	Sequence 8, Appli	
12	603.5	25.1	747	6	US-10-492-835-27	Sequence 27, Appli	
13	594.5	24.7	747	6	US-10-492-835-15	Sequence 15, Appli	
14	570.5	23.7	349	7	US-11-123-893-13	Sequence 13, Appli	
15	567.5	23.6	736	7	US-11-169-041-207	Sequence 207, Appli	
16	556.5	23.1	398	7	US-11-123-893-11	Sequence 11, Appli	
17	546.5	22.7	357	7	US-11-123-893-12	Sequence 12, Appli	
18	448.5	18.6	769	7	US-11-072-512-2646	Sequence 2646, App	
19	298.	12.4	941	6	US-10-501-035-343	Sequence 343, App	
20	277.5	11.5	854	6	US-10-511-657-4	Sequence 4, Appli	
21	191	7.9	786	7	US-11-072-512-2944	Sequence 2944, App	
22	103	4.3	968	6	US-10-501-035-219	Sequence 219, App	
23	94.5	3.9	611	7	US-11-087-099-3358	Sequence 8358, App	
24	91.5	3.8	635	7	US-11-096-568A-29628	Sequence 29628, A	
25	91.5	3.8	710	7	US-11-096-568A-29627	Sequence 29627, A	

ALIGNMENTS

RESULT 1
 US-11-226-701-4
 Sequence 4, Application US/11226701
 Publication No. US20060009632A1
 GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Robison, Keith E.
 ; APPLICANT: White, David
 ; APPLICANT: Williamson, Mark W.
 ; APPLICANT: Cook, William James
 ; APPLICANT: Meyer, Rachel E.
 ; APPLICANT: MacBeth, Kyle J.
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Chun, Miyoung
 ; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
 ; TITLE OF INVENTION: 55092 AND 10118 MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MP-03-0210NMN
 CURRENT APPLICATION NUMBER: US/11/226,701
 CURRENT FILING DATE: 2005-09-14
 PRIORITY APPLICATION NUMBER: US/10/386,414
 PRIORITY FILING DATE: 2003-03-11
 PRIORITY APPLICATION NUMBER: 09/426,282
 PRIORITY FILING DATE: 1999-10-25
 PRIORITY APPLICATION NUMBER: 09/668,266
 PRIORITY FILING DATE: 2000-09-22
 PRIORITY APPLICATION NUMBER: 09/330,970
 PRIORITY FILING DATE: 1999-06-11
 PRIORITY APPLICATION NUMBER: 09/724,599
 PRIORITY FILING DATE: 2000-11-28
 PRIORITY APPLICATION NUMBER: 09/860,193
 PRIORITY FILING DATE: 2001-05-16
 PRIORITY APPLICATION NUMBER: 09/571,689
 PRIORITY FILING DATE: 2000-05-16
 PRIORITY APPLICATION NUMBER: 10/283,023
 Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-11-226-701-4

Query Match 93.8%; Score 2258; DB 7; Length 502;
 Best Local Similarity 100.0%; Pred. No. 9 2e-201; ;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGOTGVRAERRGSYSPIDFRLNNSTYSGEITKKVRLLSFORFYHASRLRG 87
 Db 80 GDIRLRGOTGVRAERRGSYSPIDFRLNNSTYSGEITKKVRLLSFORFYHASRLRG 139

Qy 88 IIPQAPLHLDDEDYLGQAHMLSKVGWNDFDIFLFDRLTNGSLVTLCHLFNTGLJHH 147
 Db 140 IIPQAPLHLDDEDYLGQAHMLSKVGWNDFDIFLFDRLTNGSLVTLCHLFNTGLJHH 199

Qy 148 FKLDNVTLRFLVNVQEDTHSQNPHNAWADTVQAMFCYLKEPKLASFLPDLIMGL 207
 Db 200 FKLDNVTLRFLVNVQEDTHSQNPHNAWADTVQAMFCYLKEPKLASFLPDLIMGL 259

Qy 208 LAAAHDVDPGYNQNPFLIKTNHHLANLYQNMSTLENHWRSTGMURSRLLAHLPKEM 267
 Db 260 LAAAHDVDPGYNQNPFLIKTNHHLANLYQNMSTLENHWRSTGMURSRLLAHLPKEM 319

Qy 268 TQDEQQLSSLATDINQNEFLTRKLHANKDLRLEDAQRHFMQLALKCADICNP 327
 Db 320 TQDEQQLSSLATDINQNEFLTRKLHANKDLRLEDAQRHFMQLALKCADICNP 379

Qy 320. CRWEMSKQWSERVICEFRQGLEQKFPELISPLCNCQKDSPSIQTGFMSVIVEPLFR 387
 Db 380 CRWEMSKQWSERVICEFRQGLEQKFPELISPLCNCQKDSPSIQTGFMSVIVEPLFR 439

Qy 388 EWAHTGNSTLSENMLGHIAHNKAQWKSLLPRHRSRGSSGPDHDIAGQGTSESOEG 447
 Db 440 EWAHTGNSTLSENMLGHIAHNKAQWKSLLPRHRSRGSSGPDHDIAGQGTSESOEG 499

Qy 446 DSP 450
 Db 500 DSP 502

Query Match 53.2%; Score 1280; DB 7; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.3e-110; ;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GDIRLRGOTGVRAERRGSYSPIDFRLNNSTYSGEITKKVRLLSFORFYHASRLRG 87
 Db 80 GDIRLRGOTGVRAERRGSYSPIDFRLNNSTYSGEITKKVRLLSFORFYHASRLRG 139

Qy 88 IIPQAPLHLDDEDYLGQAHMLSKVGWNDFDIFLFDRLTNGSLVTLCHLFNTGLJHH 147
 Db 140 IIPQAPLHLDDEDYLGQAHMLSKVGWNDFDIFLFDRLTNGSLVTLCHLFNTGLJHH 199

Qy 148 FKLDNVTLRFLVNVQEDTHSQNPHNAWADTVQAMFCYLKEPKLASFLPDLIMGL 207
 Db 200 FKLDNVTLRFLVNVQEDTHSQNPHNAWADTVQAMFCYLKEPKLASFLPDLIMGL 259

Qy 208 LAAAHDVDPGYNQNPFLIKTNHHLANLYQNMSTLENHWRSTGMURSRLLAHLPKEM 267
 Db 260 FKLDNVTLRFLVNVQEDTHSQNPHNAWADTVQAMFCYLKEPKLASFLPDLIMGL 259

Qy 268 LAAAHDVDPGYNQNPFLIKTNHHLANLYQNMSTLENHWRSTGMURSRLLAHLPKEM 267
 Db 260 LAAAHDVDPGYNQNPFLIKTNHHLANLYQNMSTLENHWRSTGMURSRLLAHLPKEM 319

Qy 268 T 268
 Db 320 T 320

RESULT 3
 US-11-091-018-10
 Sequence 6, Application US/11091018
 Publication No. US2005028755A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Robison, Keith E.
 APPLICANT: White, David
 APPLICANT: Williamson, Mark W.
 APPLICANT: Cook, William James S.
 APPLICANT: Meyers, Rachel E.
 APPLICANT: MacBeth, Kylie J.
 APPLICANT: Carroll, Joseph M.
 APPLICANT: Chun, Miyoung
 TITLE OF INVENTION: NOVEL 55092 AND 10218 MOLECULES AND USES THEREFOR
 FILE REFERENCE: MP103_0310NIM
 CURRENT APPLICATION NUMBER: US/11/226-701
 CURRENT FILING DATE: 2005-09-14
 PRIOR APPLICATION NUMBER: US/10/386,414
 PRIOR FILING DATE: 2003-03-11
 PRIOR APPLICATION NUMBER: 09/426,282
 PRIOR FILING DATE: 1999-10-25
 PRIOR APPLICATION NUMBER: 09/668,266
 PRIOR FILING DATE: 2000-09-22
 PRIOR APPLICATION NUMBER: 09/330,970
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: 09/724,599
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 09/860,193
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 09/571,689
 PRIOR APPLICATION NUMBER: 10/283,023

RESULT 4.0
 US-11-091-018-10
 Sequence 10, Application US/11091018
 Publication No. US2005028755A1
 GENERAL INFORMATION:
 APPLICANT: Gretaradottir, Solveig
 APPLICANT: Thordalffson, Guðmar
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
 TITLE OF INVENTION: METHODS OF TREATMENT
 FILE REFERENCE: 2345_2010-16
 CURRENT APPLICATION NUMBER: US/11/091,018
 CURRENT FILING DATE: 2005-03-25
 PRIOR APPLICATION NUMBER: US/10/386,414
 PRIOR FILING DATE: 2003-09-25
 PRIOR APPLICATION NUMBER: 10/255,120
 PRIOR FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: 10/419,723
 PRIOR FILING DATE: 2003-04-18
 PRIOR APPLICATION NUMBER: 10/650,120
 PRIOR FILING DATE: 2003-08-27
 PRIOR APPLICATION NUMBER: 10/067,514
 PRIOR FILING DATE: 2002-02-04
 PRIOR APPLICATION NUMBER: 09/811,352
 PRIOR FILING DATE: 2001-03-19
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 10
 LENGTH: 507
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-091-018-10

Query Match 25.1%; Score 604.5; DB 7; Length 507;

Best Local Similarity 33.3%; Pred. No. 6.8e-48;
Matches 133; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KCKVKRLLS---FORYFAASRLRGITIQAFLPLDILGQARHMLSKVGMWDFD.FPL 121
Db 52 KEKCKKRPMOSISGVKKLMMSSLTNSSIREFGVKTEQEVLAKE--LEDVNKGHLAVR 108

Qy 122 FDRLTNGNSLVTLICH-LPNTNGLJHHFKLDMTLLHRFLYMDQHSONPYRNAVAHAAD 180
Db 109 IAEL-SGNRPLTVIMHTIQERDLIKTRKIPDVTLITYLMTLEDHYHDVAYINNIHAAD 245

Qy 181 VTOQMHCYLKEPKLASFLTPLDIMGLLAAAAGHDVDHPGVNOFLIKTNHHLANLYQNMIS 240
Db 246 VVOSTHVLISTPALEAVFTDLEIAIAFASA1HDVHDGVSNOLINTNSELALMYNDSS 305

Qy 241 VLENHHWSTIGMRESR -LLAHLPKEMTODIEQQLGSLILATDINRQNEFLTRLKHL 298
Db 306 VLENHHLAVGKFLLQEENCDFONLTKKOROSLRKVMIVDILATDMSKHMNLADLKTMV 365

Qy 299 HNKD----LRLEDAQDRHFMQLQIALKCADICNPCTWEMSKOWSERVCEEFPRQGELE 352
Db 366 ETAKVTTSSGVLLDNYSBRIQVQNMVHACDLNSNPTELQLYROWTDRLMEEFPRQGDR 425

Qy 353 QKPELEISPLCNQOKDSIPISQIGFMSYIVEPLFREWAHTGNSTLSENMLGHIAHNKAQ 412
Db 426 RERGMEISMCDKHNASTVKSQVGPIDIVHPLMWTADLVHPD-AQDILDTLDNREW 483

Qy 413 WKSILPQRHRSRGSSGSPDPDHAGQTESE-----EQEGDS 449
Db 484 YQSTIPQ-----SPSPAPDDPEEGQGQTEKEQFLTELEDGES 522

RESULT 5
US-11-091-018-6

Qy 353 QKPELEISPLCNQOKDSIPISQIGFMSYIVEPLFREWAHTGNSTLSENMLGHIAHNKAQ 412
Db 348 RERGMEISMCDKHNASTVKSQVGPIDIVHPLMWTADLVHPD-AQDILDTLDNREW 405

Qy 413 WKSILPQRHRSRGSSGSPDPDHAGQTESE-----EQEGDS 449
Db 406 YQSTIPQ-----SPSPAPDDPEEGQGQTEKEQFLTELEDGES 444

RESULT 4
US-11-091-018-9

Sequence 9 Application US/11091018
Publication No. US20050287551A1

GENERAL INFORMATION:
APPLICANT: Gretarsdottir, Solveig
APPLICANT: Thorleifsson, Guðmar
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
METHODS OF TREATMENT
FILE REFERENCE: 2345, 2010-016

CURRENT APPLICATION NUMBER: US/11/091,018
PRIORITY APPLICATION NUMBER: PCT/US03/29906
PRIORITY FILING DATE: 2003-09-25
PRIORITY APPLICATION NUMBER: 10/255,120
PRIORITY FILING DATE: 2002-09-25
PRIORITY APPLICATION NUMBER: 10/419,723
PRIORITY FILING DATE: 2003-04-18
PRIORITY APPLICATION NUMBER: 10/650,120
PRIORITY FILING DATE: 2003-08-27
PRIORITY APPLICATION NUMBER: 10/067,514
PRIORITY FILING DATE: 2002-02-04
PRIORITY APPLICATION NUMBER: 09/811,352
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 673
TYPE: PRT
ORGANISM: Homo sapiens
US-11-091-018-6

Query Match 25.1%; Score 604.5; DB 7; Length 673;
Best Local Similarity 33.3%; Pred. No. 9.9e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKCKVRLLS---FQRYPHASRLRGLIPQAPLHLDDEYLQARHMLSKVGMWDFD.FPL 121
Db 218 KEKCKKRPMOSISGVKKLMMSSLTNSSIREFGVKTEQEVLAKE--LEDVNKGHLAYER 274

Qy 122 FDRLTNGNSLVTLICH-LPNTNGLJHHFKLDMTLLHRFLYMDQHSONPYRNAVAHAAD 180
Db 275 IAEL-SGNRPLTVIMHTIQERDLIKTRKIPDVTLITYLMTLEDHYHDVAYINNIHAAD 333

Qy 181 VTOQMHCYLKEPKLASFLTPLDIMGLLAAAAGHDVDHPGVNOFLIKTNHHLANLYQNMIS 240
Db 334 VVOSTHVLISTPALEAVFTDLEIAIAFASA1HDVHDGVSNOLINTNSELALMYNDSS 393

Query Match 25.1%; Score 604.5; DB 7; Length 585;
Best Local Similarity 33.3%; Pred. No. 8.2e-48;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KCKVKRLLS---FORYFAASRLRGITIQAFLPLDILGQARHMLSKVGMWDFD.FPL 121
Db 130 KEKCKKRPMOSISGVKKLMMSSLTNSSIREFGVKTEQEVLAKE--LEDVNKGHLAVR 186

QY 241 VLENHWRSTIGMLRESR -LLAHLPKEMTDQIEQQGLSLILATDINRONEFLTRK AHL 298
 Db 394 VLENHHLAVGFKLQEENDIFQNLTKRQSLRKMVIDIVLATDMSKHMNLLADKTMV 453
 QY 299 HNKD -----LRLEDAQDRHFMQLTALKACDINCNPCTIWIEMSKOWSERVCEBFYRG E 352
 Db 454 ETKKVTSSGVLLDNYSDRIQVLIQNMVKHADLSNPTKPPQLYQWTDRIMEEFRQGD R 513
 QY 353 QKPELEISPLCNCQKDSISI1QGFMSYIVEPLFREWAHTGNSTSENMIGHLAHNKAQ 412
 Db 514 RERGMEISPMCNDKINASVKSQVGDYDITVHPLMWTADLVHPD -AQDILDLEDNEW 571
 Qy 413 WKSLLPRQRSGSSGGDHDHAGQGTSE-----EQEGDS 449
 Db 572 YQSTIPQ-----SPSPADDPEBGRGQTEKFQFELTEDGES 610
 RESULT 6
 US-11-091-018-4
 ; Sequence 8 Application US/11091018
 ; Publication No. US20050287551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gretaarsdottir, Solveig
 ; ATTORNEY: Thorleifsson, Guðmar
 ; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
 ; TITLE OF INVENTION: METHODS OF TREATMENT
 ; FILE REFERENCE: 2345 - 2010-016
 ; CURRENT APPLICATION NUMBER: US/11/091,018
 ; CURRENT FILING DATE: 2005-03-25
 ; PRIOR APPLICATION NUMBER: PCT/US03/29906
 ; PRIOR FILING DATE: 2003-09-25
 ; PRIOR APPLICATION NUMBER: 10/255,120
 ; PRIOR FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: 10/419,723
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: 10/650,120
 ; PRIOR FILING DATE: 2003-08-27
 ; PRIOR APPLICATION NUMBER: 10/067,514
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 03/811,352
 ; PRIOR FILING DATE: 2001-03-19
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 745
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-091-018-4

Query Match 25.1% Score 604.5; DB 7; Length 745;
 Best Local Similarity 33.3%; Pred. No. 1.1e-17;
 Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRILS---FORYFHASRLRLRGSIPOALPHLDDEDYLQARHMLSKYGMWDFDIFL 121
 Db 290 KKKVKRILSQQSGVKKLHMSSLTNSSSPRLKIPDVLAK--LEDVNKGHLVFR 346
 QY 122 FDRLTNGSLVTLCH_LFNTHGLIHFKLDMVTFQFLKIPDVLTLTYMLTLEDHTHADYAHNNHAAD 180
 Db 347 IAEL-SGNRPLTVIMTTIQFRDLUFTFKIPDVLTLTYMLTLEDHTHADYAHNNHAAD 405
 QY 181 VTQAMHCYKLBPKLASPLTPDLMGLLAAAHDVPGVNPQFLKTNNHLANLYONMS 240
 Db 406 VVQSTHVLSSPALEAVFTDLEILAAIFASA1HDVTHPGVSNQFLNTNSEALMYNDSS 465
 QY 241 VLENHHRSTIGMLRESR -LLAHLPKEMTDQIEQQGLSLILATDINRONEFLTRKAHL 298
 Db 466 VLENHHLAVGFKLQEENDIFQNLTKRQSLRKMVIDIVLATDMSKHMNLLADKTMV 525
 QY 181 VTQAMHCYKLBPKLASPLTPDLMGLLAAAHDVPGVNPQFLKTNNHLANLYONMS 240
 Db 348 VVQSTHVLSSPALEAVFTDLEILAAIFASA1HDVTHPGVSNQFLNTNSEALMYNDSS 407
 QY 241 VLENHHRSTIGMLRESR -LLAHLPKEMTDQIEQQGLSLILATDINRONEFLTRKAHL 298
 Db 408 VLENHHLAVGFKLQEENDIFQNLTKRQSLRKMVIDIVLATDMSKHMNLLADKTMV 467
 Qy 299 HNKD -----LRLEDAQDRHFMQLTALKACDINCNPCTIWIEMSKOWSERVCEBFYRG E 352
 Db 526 ETKKVTSSGVLLDNYSDRIQVLIQNMVKHADLSNPTKPPQLYQWTDRIMEEFRQGD R 585
 Qy 353 QKPELEISPLCNCQKDSISI1QGFMSYIVEPLFREWAHTGNSTSENMIGHLAHNKAQ 412
 Db 586 RERGMEISPMCNDKINASVKSQVGDYDITVHPLMWTADLVHPD -AQDILDLEDNEW 643
 Qy 413 WKSLLPRQRSGSSGGDHDHAGQGTSE-----EQEGDS 449

RESULT 8

Db 644 YQSTIPQ----SPSAPDPPEGRQQTEKFQFELTIEEDGES 682 US-10-492-835-12

Query Match 25.1%; Score 604.5; DB 6; Length 748;
Best Local Similarity 33.3%; Pred. No. 1.e-47;
Mismatches 151; Indels 33; Gaps 9;

/ Sequence 12, Application US/10492835
/ Publication No. US20050289660A2
GENERAL INFORMATION.
/ APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
/ TITLE OF INVENTION: CYCLIC AMP PHOSPHODESTERASE 4D7 ISOFORMS AND METHODS
/ CURRENT APPLICATION NUMBER: US/10/492,835
/ CURRENT FILING DATE: 2004-04-15
/ FILE REFERENCE: MEMORY 4 WO
/ SEQ ID NO 12.
/ LENGTH: 748
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-492-835-12

Query Match 25.1%; Score 604.5; DB 6; Length 748;
Best Local Similarity 33.3%; Pred. No. 1.e-47;
Mismatches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVKRLLS---PQRYPHASRLRGITIPOAPHLILDEPDYLGARHMLSKVGMWDFDFL 121
Db 293 KEKKKRPMQSISGYKLMHSSSLNTNSSPRFGVKTEQDVLAKE--LEDVNKGGLAYER 349

Qy 122 FDRLTNGNSVLTLICH-LFNTNGLHPLMTLHFRFLYWDYHSQNPYNAVHAD 180
Db 350 IAEI-SGRPLTVIMHTFQERDLKTFKIPVDTLITYLTDHYDAVAYINNIHAD 408

Qy 181 VTQAMHCYKKEPKLASFLTPLDIMGLIAAAAHVDHPGVNQPLIKTNHHLANLYOMS 240
Db 409 VVQSTHVLLSTPALEAVFTDLEIAIFASAIDVHDGVSNQPLINTSELALMYNDSS 468

Qy 67 KKKVKRLLS---PQRYPHASRLRGITIPOAPHLILDEPDYLGARHMLSKVGMWDFDFL 121
Db 293 KEKKKRPMQSISGYKLMHSSSLNTNSSPRFGVKTEQDVLAKE--LEDVNKGGLAYER 349

Qy 122 FDRLTNGNSVLTLICH-LFNTNGLHPLMTLHFRFLYWDYHSQNPYNAVHAD 180
Db 350 IAEI-SGRPLTVIMHTFQERDLKTFKIPVDTLITYLTDHYDAVAYINNIHAD 408

Qy 181 VTQAMHCYKKEPKLASFLTPLDIMGLIAAAAHVDHPGVNQPLIKTNHHLANLYOMS 240
Db 409 VVQSTHVLLSTPALEAVFTDLEIAIFASAIDVHDGVSNQPLINTSELALMYNDSS 468

Qy 241 VLENHHRWSTIGMRESR-LLAHLPKEMTDIEQQLGSLILATDINRQNENPLTRKHL 298
Db 469 VLENHHLAVGFKLUQEENCDIFQNLTKKQROSURKMYDIVLATDMSGHMLLAHKNAQ 528

Qy 299 HNKD-----LRLEDAQRHFMQLQALKCADICNPCTWEMSKQWERVICEEFPYRGEB 352
Db 529 ETKKVTSSGVLLDNYSDRIVQVNMVTCADLSNPTEPLQLFRTWDRIMEEFRRQGDRE 588

Qy 353 QKFELEISPLCNQKDSIPIQGMSYIIVEPFLREWAHTGNSTLSENMGLHAKNAQ 412
Db 589 RERGMIEISPMCDRHNASTEKVSQVGFIDTVHPLWETADLVHFD-AQDILDTLEDNREW 646

Qy 413 WKSLLPROHRSRSSSGSPDHDHAGQTSEB-----EQEGDS 449
Db 647 YQSTIPQ-----SPSPAPDPPEGRQQTEKFQFELTIEEDGES 685

RESULT 10

Db 409 VVQSTHVLLSTPALEAVFTDLEIAIFASAIDVHDGVSNQPLINTSELALMYNDSS 468 US-11-091-018-2

; Sequence 2, Application US/11091018 .
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Grettarson, Solveig
; APPLICANT: Thorelfsson, Guðmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010.016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-2

Query Match 25.1%; Score 604.5; DB 7; Length 809;
Best Local Similarity 33.3%; Pred. No. 1.e-47;
Mismatches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

Qy 66 KKKVKRLLS---PQRYPHASRLRGITIPOAPHLILDEPDYLGARHMLSKVGMWDFDFL 121

RESULT 11
US-10-492-835-8
; Sequence 8 Application US/10492835
; Publication No. US2005028966042
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 8
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-492-835-8

Query Match 25.1%; Score 603.5; DB 6; Length 747;
Best Local Similarity 33.3%; Pred. No. 1.4e-47;
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

Db 589 RERGMELSPMCDKHNASVEKSQVGFIDYVHPLWETADLVHPD-AQDILDLTLEDNREW 646
Qy 413 WKSLLPQRHRSRGSSGSGPDDHAGQTESE-----EQEGDS 449
Db 647 YQSTRIPQ-----SPSPAPDDQEDGQQTKEFQFELTLEEDGES 685

RESULT 12
US-10-492-835-27
; Sequence 27 Application US/10492835
; Publication No. US2005028966042
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 27
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-492-835-27

Query Match 25.1%; Score 603.5; DB 6; Length 747;
Best Local Similarity 33.3%; Pred. No. 1.4e-47;
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

Db 66 KKVKVKRULS---FQRYPHASRLRGITPOAQLHLDEDYLQARHMLSKVGMWDFIFL 121
Qy 293 KKKKPKRPSOISGVKLHMSLTSNTSPRKVTKEDVLAKE--LEDYWKWGLFVER 349
Db 293 FDLTLTNSLVLCH-LFNTHGLLHFQKLDMVTLRFLVQEDYHSQNPHNAVAAD 180
Qy 350 IAEL-SGNRPLTVMTMIFQERDLKLFKIPVDTLTYLMTLEDHTHADVAHNNAHAAD 408
Db 181 VTOAMHCYLKPKLASFLPDIMGLHAAAHDVHPGVNQPFLLKTNHHLANLYONMS 240
Qy 409 VVQSTHVLSTPALEAVFTDLEIAIAFASA1HDVHPGVSNQFLNTSELALMNDSS 468
Db 241 VLENHHWRSTIGMLRESR-LLAHKPEMTQDIEQOLGSILATDINRNQBEFLTRKAHL 298
Qy 469 VLENHHHLAVGFKLQOBNCDFQNLTKKQROSRLKQADIVLATDKHNNLLADKTMV 528
Db 299 HNKD----LRLEDADQRHFMQLQALKCADICNPRIWENSKOMSERVCEEFYRCQEL 352
Qy 529 ETKKVTVSSGVLLDNYSDRIQVLMNVHCAIDSNPTKPLQYRONTDRIMEFFRQGDRE 588
Db 353 QKFELIESPLCNQOKDOSPISTIQGMWSYIVEPLFRWAHFTGNSTLSENMGLHAINKAQ 412
Db 589 RERGMELSPMCDKHNASVEKSQVGFIDYVHPLWETADLVHPD-AQDILDLTLEDNREW 646
Qy 413 WKSLLPQRHRSRGSSGSGPDDHAGQTESE-----EQEGDS 449
Db 647 YQSTRIPQ-----SPSPAPDDQEDGQQTKEFQFELTLEEDGES 685

RESULT 13
US-10-492-835-15
; Sequence 15 Application US/10492835
; Publication No. US2005028966042
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 15
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-492-835-15

Query Match 25.1%; Score 603.5; DB 6; Length 747;
Best Local Similarity 33.3%; Pred. No. 1.4e-47;
Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

Db 66 KKVKVKRULS---FQRYPHASRLRGITPOAQLHLDEDYLQARHMLSKVGMWDFIFL 121
Qy 293 KKKKPKRPSOISGVKLHMSLTSNTSPRKVTKEDVLAKE--LEDYWKWGLFVER 349
Db 122 FDLTLTNSLVLCH-LFNTHGLLHFQKLDMVTLRFLVQEDYHSQNPHNAVAAD 180
Qy 350 IAEL-SGNRPLTVMTMIFQERDLKLFKIPVDTLTYLMTLEDHTHADVAHNNAHAAD 408
Db 181 VTOAMHCYLKPKLASFLPDIMGLHAAAHDVHPGVNQPFLLKTNHHLANLYONMS 240
Qy 409 VVQSTHVLSTPALEAVFTDLEIAIAFASA1HDVHPGVSNQFLNTSELALMNDSS 468
Db 241 VLENHHWRSTIGMLRESR-LLAHKPEMTQDIEQOLGSILATDINRNQBEFLTRKAHL 298
Qy 469 VLENHHHLAVGFKLQOBNCDFQNLTKKQROSRLKQADIVLATDKHNNLLADKTMV 528
Db 299 HNKD----LRLEDADQRHFMQLQALKCADICNPRIWENSKOMSERVCEEFYRCQEL 352
Qy 529 ETKKVTVSSGVLLDNYSDRIQVLMNVHCAIDSNPTKPLQYRONTDRIMEFFRQGDRE 588
Db 353 QKFELIESPLCNQOKDOSPISTIQGMWSYIVEPLFRWAHFTGNSTLSENMGLHAINKAQ 412
Qy 533 QKFELIESPLCNQOKDOSPISTIQGMWSYIVEPLFRWAHFTGNSTLSENMGLHAINKAQ 412

Db 653 QSMIFQ-----SBSPPLDEQNRCQGLMEKFQFELTDEEDSEGPEKEGE 697

Search completed: March 10, 2006, 20:23:10
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